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arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence encodes a human scavenger receptor, designated SRCL-P1. The SRCL-P1 polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic complications, bacterial infection and restenosis following angioplasty, which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Scavenger receptor proteins SRCL-P1 with collectin-like structure, useful for treatment and diagnosis of diseases associated with oxidized low-density lipoprotein accumulation
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                                                                                                                          AAGTGGCTGGATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAAC
                                                                           TGGGGTCATGGCCCAGGAGAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGG
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                                                                                                                                                                                                                                                                                Nucleotide sequence of a human scavenger receptor.
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rheumatoid arthritis; gene;
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                                                                                                                                                                                                                                                                  The invention relates to a human scavenger receptor-like protein. protein is useful as a target molecule for diagnosis, prevention treatment of autoimmune diseases such as rheumatoid arthritis.
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                                                                                                                                                                        New scavenger receptor-like protein for diagnosis, prevention treatment of autoimmune disease, such as rheumatoid arthritis
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Pred. No. 0;
0; Mismatches
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Best Local Similarity 99.9%;
Matches 1694; Conservative 0
2000JP-0375066
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P-PSDB; ABB08642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-5, EXMAD-4, EXMAD-5, EXMAD-6, EXMAD-7, EXMAD-10, EXMAD-11, EXMAD-11, EXMAD-13, EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-17, EXMAD-19, EXMAD-20, EXMAD-21, EXMAD-21, EXMAD-23, EXMAD-24 and EXMAD-25. They are useful in the prevention and treatment of cancers, cell proliferation, cardiovascular, reproductive, immune, musculoskeletal, developmental an qastrointestinal disorders and inflammation.
                                                                                                                                                                                                                                                                                                                        DAM;
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                                                                                                                                                                                                                                                                                                                                                                                                  Isolated polynucleotide encoding extracellular matrix or adhesion-associated protein (EXMAD) useful for diagnosing, treating, preventing disorders associated with expression of EXMAD such as proliferative, immune and genetic disorders
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                                                                                       cancer;
                                                                                   Extracellular matrix and adhesion-associated protein; EXMAD; cance:
infilammetion; reproductive disorder; cardiovascular disorder;
immune disorder; musculoskeletal disorder; developmental disorder;
gastrointestinal disorder; cell proliferation disorder; ss.
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Pred. No. 0;
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                                                            Human EXMAD-14 coding sequence SEQ ID NO:
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llarity 99.9%;
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Matches 1694;
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Azimzai Y;
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AAC66903 standard; cDNA; 2641

AAC66903 ID AAC6

RESULT

CTGTCATCTGCATTA

AAGTCTTCACATCTTGTTTTCATAAACACTAGAGGAACAGCAATGGATAAAAAACAG

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       CACACAGATGATCTGACCTCCTTGAATAATACCCTGGCCAACATCCGTTTGGATTCTGTT
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Human; cytostatic; antirheumatic; antiarthritic; vulnerary; analgesic; antiflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; noctropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Allaheimer's disease; Parkinson's disease; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss.
                                                                                                                                                                                    AACGATTTCCAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTA 1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polynucleotide encoding the of neurological disorders,
                                           AACGATTTCCAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTA
                                                                           AAGTGGCTGGATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAAC
                                                                                      TGGGGTCATGGCCCAGGAGAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGG
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Spaulding V;
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MERBERG D.
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or liver fibrosis autoimmune diseases, bone disorders and lung 

Claim 250; Page 231-232; 284pp; English

The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic acid (CDNA) inserts (II), where the protein is substantially free from cother mammalian proteins. (I) are useful for preventing, treating or ameliorating a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, call differentiation, antinifiammatory, stem cell growth factor activity and activin or inhibin-related activities. (I) can be used to manipulate stem cells in culture to give crise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic discorders. (I) induces the proliferation of neural cells and cells and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzhelmer's, parkinson's disease, amycriophic cativity, regulation of haematopoiesis and is useful for the treatment of activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as throndocytopaenia and for regeneration of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as throndocytopaenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve for treating osteoporosis, osteoarthritis, bone degeneration of accordance of its also useful for gut protection or periodortal disease. (I) is also useful for gut protection or cegeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, ulcers, diabetes mellitus, mysathenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is a bone degeneration and conditions, such as asthma or other respiratory pro sequence is that of a polynucleotide of the invention

Sequence 2929 BP; 901 A; 699 C; 692 G; 637 T; 0 other;

Gaps DB 24; Length 2929; Indels <del>,</del>, Score 1681.4; Pred. No. 0; 0; Mismatches 99.2%; 99.9%; Best Local Similarity 99.9 Matches 1693; Conservative Query Match

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657 9 GTCACGAATCTGCAGCAAGATACCAGCGTGCTCCAGGGCAATCTGCAGAACCAAATGTAT Н ŏ 엽

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180 AACCTCATCACGAATCTGCAGCGGTCTGTGGATGACACAAGCCAGGCTATCCAGCGAATC AACCTCATCACGAATCTGCAGCGGTCTGTGGATGACACAAGCCAGGCTATCCAGCGAATC 717 121 οy ga

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CTGAAGGAGAAAGTGCAGAGCTTGCAGACGCTGCCTGCCAACACTCTGCGTTGGCCAAA 837 241

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1556 1020 1616 2036 1316 780 TCAGTGATTATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAAT 1376 CCCGGCCCTCAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGG 1140 GTGCCTGGACCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCCATGCCAGGCCCCAAG 1200 GGCCCCCCCCGGCCCTCCTGGCCCATCAGGAGCGGTGCTGCCCCTGGCCCTGCAGAATGAG 1260 CCAACCCCGGCACCGGAGGACAATGGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAA 1320 TGCTACTATTTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGAC 1976 AAGTGGCTGGATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAAC 1560 99 720 840 900 96,0 540 TITACAATACTACAAGGTCCACCGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAG TCTCTCAGGATGCAACAAGATTTGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTA TCAGTGATTATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAAT CCTGCCCCTGCGGGTGAGAGGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGC CTCTTTGAGACGGATATTGTGAACATCATTAGCAATATCAGTTACAGCCCACCTG TTTACAATACTACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAG GGCCCTCAGGGCCCCCAGTGGGGACCCAGGCCCCCGGGGCCCACCAGGCAAAGAGGGGACTC AAGTCTTCACATCTTGTTTTCATAAACACTAGAGGAACAGCAATGGATAAAAAAAGAG CACACAGATGATCTGACCTCCTTGAATAATACCCTGGCCAACATCCGTTTGGATTCTGTT CCTGCCCTGCGGGTGAGAGAGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGC GGCAAAGGATCTAAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCC CTCTTTGAGACGGATATTGTGAACATCATTAGCAATATCAGTTACACAGCCCACCACGTG CGGACGCTGACCAGCAATCTAAATGAAGTCAGGACCACTTGCACAGATACCCTTACCAAA 1077 1137 1617 1141 1201 1797 1857 1321 1977 1441 2037 1257 1557 1081 1737 1261 1917 1381 481 1197 661 721 1317 781 1377 1437 901 1497 1021 1501 601 961 g οχ Q ò qq δ q òγ qq Ω g g ò Dβ ò qq ò g οy g ò Q δ qq ŏ QQ δλ q ŏ a õ ò g ô qq οy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence encodes a human secreted protein of the invention. This DNA sequence was isolated from a human adult brain cDNA library, and was designated clone bv227_1. The DNAs and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in
                                                                                                                                                                                                                              Secreted protein; human; nutritional supplements; immune stimulant; immune suppressor; haematopoiesis regulator; tissue growth; chemotaxis; activin/inhibin; chemokinesis; haemostasis; thrombolysis; receptor/ligand activity; anti-inflammatory; tumour inhibitor; cadherin/tumour invasion suppressor; ds.
                                             1680
                                                      proteins - derived from
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        TGGGGTCATGGCCCATGGCCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGG
                         2157 TGGGGTCATGGCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGG
                                             AACGATTTCCAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTA
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Spaulding
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9705-0868696.
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9705-0869193.
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                                                                                  CTGTCATCTGCATTA 1695
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04-JUN-1997;
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humans and animals, although no supporting data is given. Suggested activities include nutritional sources or supplements, immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, rehemotatic/chemokinetic activity, haemastatic and thrombolytic activity, receptor/ligand activity, and tumour inhibition activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The DNAs are also stated to be useful for gene therapy. A host cell transfected with the DNA, or its subframents and variants is useful for recombinant production of the human secreted protein clones.
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99.9%; Pred No. 0;
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Matches 1693; Conservative
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                       CCTGGCCCTGCGGGTGAGAGAGGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGC
                                              GGCAAAGGATCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCC
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peripheral nervous system; neuropathy; central nervous system;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to creat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous allocalised neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activity, inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
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Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
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Zhang J
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Yang Y,
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Xu C, Xue AJ,
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Pred. No. 0;
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system injuries
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Wehrman T, Xu
Goodrich R,
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2000US-0552317.
2000US-059042.
2000US-0653450.
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Best Local Similarity 99.9
Matches 1674; Conservative
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P-PSDB; AAM41472.
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Wang Z,
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09-JUL-2000; 2
19-JUL-2000; 2
03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang
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                    AGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTT
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                                       TCATAAACACTAGAGGAACAGCAATGGATAAAAAAACAGATGGTAGGGAGAGAGGCC
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Yang Y,
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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system injuries
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P-PSDB; AAM39686.
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14-SEP-2000;
19-OCT-2000;
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Claim 1; SEQ ID NO 1045; 10078pp; English

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Human angiogenesis related cDNA PRO7223 SEQ ID NO:
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         The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM4213) with noctropic, immunosuppressant and cytostatic activity. The polynuclectides are useful in gene therapy. A composition containing a polypeptide or polynuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system, such as peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Sydrome other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotratic/chemokinetic activity, hamotratic/chemokinetic activity, damotratic/chemokinetic activity, damotratic/chemokinetic activity, damotratic/chemokinetic activity, damotratic/chemokinetic activity, arthritis and inflammation, leukaemias and
                                                                                                                                                              The sequence data for this patent did not form part of the printed
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CCACCGGGCCCCAGGGGTCCAAGAGGTGAACAGAGGATCCCAGGGACCCCCTGGCCCAACT
                                                                                                                                                                                                      AGAGGCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAAGGC
                                                                                                                                                                                                                                                                               TCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGT
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thrombophiebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                              200 TGCAGCAGGTTTTTCTTCAAGCCAAGAAGGACACGGATTGGCTGAAGGAGAAAGTGCAGA 259
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                                           hundred and eighty seven nucleic acids encoding PRO polypeptides, ful in diagnosis and treatment of cardiovascular (e.g. myocardial
                                                      infarction), endothelial or angiogenic disorders in a mammal -
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                                                                                                     Claim 1; Fig 27; 567pp; English
                                                                                                                                                                                                                                                                                                                                 Matches 1491; Conservative
 2002-171999/22.
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WPI; 2002-171999,
P-PSDB; ABB95436
                                                             useful in
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              cancer;
disorder;
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   numman; anglogenesis; PRO protein; cardiovascularisation; wound; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
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2000WO-US32678.
2000WS-0747259.
2000WO-US32856.
2001US-0767609.
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2000WO-US23328.
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2001US-0802706.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
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PAONI N F.
STEPHAN J F.
WATANABE C K
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FERRARA N.
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28-JUL-2000
17-ANG-2000
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115-SEP-2000
116-SEP-2000
118-SEP-2000
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118-SEP-2000
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CTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGACCTCGGGGAC
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                                           CCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGTG
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Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; anglogenic disorder; cardiac hypertrophy, atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; themmatoid arthritis; mycoardial infarction; thrombophlebitis; lymphangitis; tumour anglogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
                                                                                                                                   Human PRO7223 cDNA sequence SEQ ID NO:27.
                  BP.
                ABL88085 standard; cDNA; 2005
                                                                                            (first entry)
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Sequence 2005 BP; 606 A; 493 C; 491 G; 415 T; 0 other;

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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85033. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic cytostatic, activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or anglogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular rehematoid arthritis, angina, mypertension, arterial restenosis, rheumatoid arthritis, angina, mypocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
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A, Pan J,
, Ye W;
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J, Hillan KJ, Marsters SA,
ZK, Williams PM, Wood WI,
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2000US-0709238.
2000WO-US30952.
2000WO-US30873.
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Godowski PJ, Gurney AL,
Stephan JF, Watanabe CK,
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P-PSDB; ABB84830.
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Godowski PJ,
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17-AUG-2000;
23-AUG-2000;
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07-SEP-2000;
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GCCCATCAGGAGCGGTGGTGCCCCTGGCCCTGCAGAATGAGCCAACCCCGGCACCGGGAGG 1279
                                                                                                            ACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCTGCATTA 1695
        ACAATGGCTGCCCCCCTCACTGGAAGAACTTCACAGACAAATGCTACTATTTTCAGTTG
                                                                                                                                   AGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTT
                                                                         ACTEGATCEGCCTCACAGACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGACAT
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92..2320
/*tag= a
/product= "scavenger
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2000JP-0309068
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                                                129 AGGATATGAACAGCCAGCTCAACTCCATTCACAGGTCAGATGGAGAACATCACTATCT
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       24;
       DB
      Score 1477.6;
Pred. No. 0;
                       0; Mismatches
      87.2%;
99.7%;
                       Conservative
              Similarity
                       Matches 1491;
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Best Local 8
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Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angloplasty;
low density lipoprotein; ss.
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Nucleotide sequence of a human scavenger receptor
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AACGATTTCCAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTA 1680
 1403 TTTACCATTCTACAAGGTCCTCCTGGCCCCAGAGGTCCAAAAGGTGACAGAGGATCTCAG 1462
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                                                                                                                 AGCAAAGGATCCAAAGGCTCACAGGGTCCCAAAGGATCTCGTGGGTCCCCAGGGAAGCCT
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                                                              CCTGGCCCTGCGGGTGAGAGAGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGC
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                      GGACCCCCTGGCCCAACTGGCAACAAGGGACAGAAAGGAGAGAAGGGGGGAGCCTGGACCA
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                           The present sequence encodes a human scavenger receptor, designated SRCL-P1. The SRCL-P1 polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic complications, bacterial infection and restenosis following angioplasty, which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products into
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                                                                                                                                  Sequence 2637 BP; 829 A; 617 C; 635 G; 556 T; 0 other;
                                                                                                                                                      Score 1359; DB 22;
Pred. No. 0;
); Mismatches 210;
           Japanese
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0
        88-93; 118pp;
                                                                                                                                                      Query Match
Best Local Similarity 87.6%;
Matches 1485; Conservative
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          Claim
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arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty; low density lipoprotein; ss.
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Pred. No. 5.1e-229;
0; Mismatches 0;
                                                                                               receptor"
                                                                                                                                                                                                                                                                                                                    Claim 4; Page 105-109; 118pp; Japanese.
                                                                                                                                                                                                                                                                                                low-density lipoprotein accumulation
                                                                                              "scavenger
                                                                Location/Qualifiers
74..1936
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Best Local Similarity 78.1%;
Matches 1323; Conservative
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                                              Homo sapiens
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disease involving abbrirant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity
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TGGGGTCATGGCCCAGGAGAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGG
                                                                                                                                     AACGATTTCCAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAAGACAGGAAGACAGTA
                                                    AAGTGGCTGGATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           forensic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #6937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 6937; 103pp; English.
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and to produce other types of data and products dependent on DNA amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the prispecification, but was obtained in electronic format directly from
                                                                                                             DB 23; Length 1521;
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                                                                                     Sequence 1521 BP; 386 A; 420 C; 425 G; 290 T; 0 other;
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                                                                                                             Score 883.8; DB 23
Pred. No. 1.5e-214;
                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                     0; Mismatches
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99.8%;
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                                                                                                                         Similarity
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1665 GCTGTGGGAGAAAAGGGGCCCTGTTGGCCCTCGAGGGTTCCCAGGCCTCAAAGGCTCAAA 1724
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                                                                         GCATGATCTTCAGTACCATACCCACTACGCCCAGAACCGCACTGTGGAGAGGTTTGAGTC 1184
                                                                                                                                                                                                                                                                      1365 CATGCTGGGCCACCACAGACCTGCTCCGGGAGCGCTTCAGCCTGCTCAGTGCCCGGCTGGA 1424
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                                             GAAAGACCTGCAGGACTTACACAAAGATGCAGAGAATAGAACAGCCATCAAGTTCAACCA
                                                                                                                                                                          TTACACAGCCCACCTGCGGACGCTGACCAGCAATCTAAATGAAGTCAGGACCACTTG
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                                                                                                                                                                     Cellular stress response protein; CSR1; CSR2; CSR3; human; macrophage; scavenger receptor protein; intracellular stress; arteriosclerosis; diabetic circulatory obstruction; microbial infection; ss.
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                                                                                                                                         Human CSR3 protein coding sequence.
                                         AAX27858 standard; DNA; 3685
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97JP-0233396
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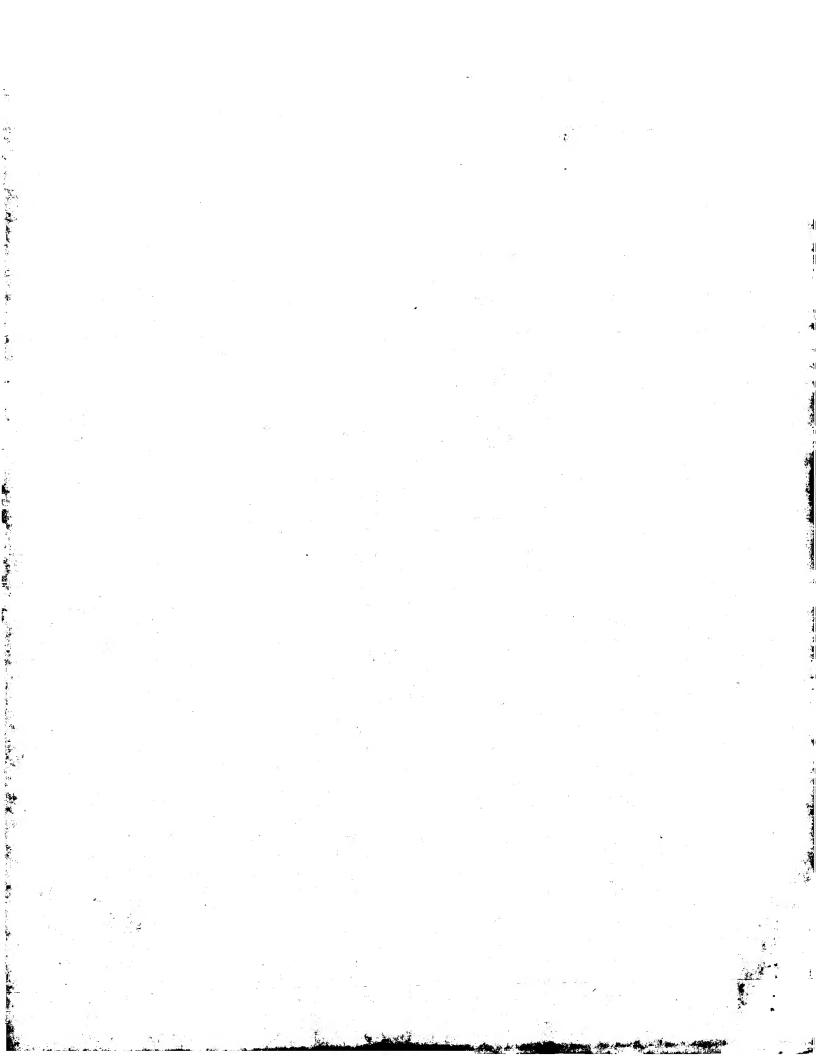
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                                                                                                                                                         (NISB ) JAPAN TOBACCO INC
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                                  1430 CACGCTGGGCTTCCACCATGCCGAGGAGCTCTACTACTACCTGAAGTCTGTCCAT 1489
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  CACAGATACCCTTACCAAACACACAGATGATCTGACCTCCTTGAATAATACCCTGGCCAA
                                                                                                                                                                                                   CACTGAAGTAGCCAACTTATCAGTGATTATGGAAGAAATGAAGCTAGTAGACTCCAAGCA
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                                                                                                    CATCCGTTTGGATTCTGTTTCTCTCAGGATGCAACAAGATTTGATGAGGTCGAGGTTAGA
                                                                                                                                                                                                                                                                                                     TGGTCAGCTCATCAAGAATTTTACAATACTACAAGGTCCACGGGCCCCAGGGGTCCAAG
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Search completed: March 21, 2003, 02:18:38 Job time : 362.008 secs



116, App 94, Appl 137, App 137, App 10, Appl Appl

Sequence Sequence Sequence Sequence

116,

Sequence Sequence

Sequence Sequence Sequence

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789 ACTACAAGGTCCACCGGGCCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCC 848
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Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: High Molecular Weight Collagen-Like
WUMBER OF SEQUENCES: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 121.6; DB 1;
Pred. No. 6.5e-23;
0; Mismatches 214;
US-09-297-269-40
US-08-159-784-1
US-09-440-879A-372
US-09-134-001C-647
US-09-134-001C-624
US-09-145-175-155-63
US-08-477-509B-98
US-08-477-509B-98
US-08-477-509B-98
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US-08-477-509B-98
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ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON
ADDRESSE: FLEHR, HOHBACH, TEST, ALBRITTON
CITY: San Francisco
CITY: San Francisco
CONTE: California
CONTE: USA
ZIP: 94111-4187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTERM I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A5555
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 494-8770
TELER: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: other nucleic
DESCRIPTION: /desc = "synth
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Best Local Similarity 53.9%;
Matches 250; Conservative
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LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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US-08-642-255-60
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   (without alignments)
   8700.356 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/BE_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
                                  version 5.1.4_p5_4578 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/ina/5A_COMB.seq:*/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-642-255-48
US-09-029-348-19
US-08-253-155A-20
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US-09-453-702B-62
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US-09-439-897-1
US-08-392-367B-1
US-08-893-467A-1
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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1156 GGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCCGGCCCT 1215
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                                                                                                                                     GGTCCACCGGGCCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCA 855
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                                               Length 756;
                                             Score 118; DB 1; Length 75
Pred. No. 5.7e-22;
0; Mismatches 200; Indels
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COUNTRY: US
ZIP: 11553
ZOMPUTER: ELOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: DILWORTH & BARRESE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08655086 Patent No. 5821089
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NAME: STEEN, JEFFER S.
REGISTRATION NUMBER: 20.063
REFERENCE/DOCKET NUMBER: 203.
TELECHONICATION INFORMATION:
TELEPHONE: 516-228-8484
TELEFRAX: 516-228-8516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOTT A.
APPLICANT: BUECHTER, DOUGLAS
APPLICANT: ZHANG, GUANGHUI
APPLICANT: CONNOLLY, KEVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32,063
                                               Query Match 7.0%;
Best Local Similarity 54.3%;
Matches 238; Conservative
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  US-08-642-255-50
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US-08-655-086-1
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                                                                                                                                                                                                                                                                                                                        1029 GGGCCCCAGTGGGGACCCAGGCCCCCCGGGCCCACCAGGCAAAGAGGGGACTCCCCGGGCC 1088
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210 ACCACCGGGTGCACCTGGCCCAGCGGGTCCGCCTGGATCTAGAGGTGACCCAGGACCGCC 269
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                                             849 TGGCCCAACTGGCAACAAGGACAGAAAGGAGAAGGGGGGAGCCTGGACCACCTGGCCC
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APPLICANT: CAPPELLO, Joseph
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS: ADDRESS: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1209 CGCCCTCCTGCCCCATCAGGAGCGGTGCCCCTGGCCCTGC 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram 1.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A5556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DESCRIPTION: /desc = "synthetic"
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; Sequence 50, Application US/08642255
; Patent No. 5773249
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LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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TOPOLOGY: lir
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REFERENCE/DOCKET NUMBER: MII-028
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                                                                                                                                                                      ; MOLECULE TYPE:
US-08-253-155A-61
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                                                                                                                                                                                                                                                                                               164 GCTTCAGGTCCCCATGGGTCCCCCGAGGTCCCCCCTGGAAAGAATGGAGATGAT 223
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                                                                                                                                         Length 3181;
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                                                                                                                                         DB 1;
                                                                                                                                       Score 113.6; DB 1
Pred. No. 1.6e-20;
                                                                                                                                                                        0; Mismatches
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02-JUN-1994
03-JUN-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/253,155
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APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Pr
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 61, Application US/08253155A Patent No. 5691147 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 36,709
                                                                                                                                      Query Match 6.7%;
Best Local Similarity 52.5%;
Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                 LENGTH: 3181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
SEQUENCE CHARACTERISTICS:
LENGTH: 3181 base pair
                                                                  TOPOLOGY: unknown ; MOLECULE TYPE: CDNA US-08-655-086-1
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565 GAAGTCAGGACCACTTGCACAGATACCCTTACCAAACACACAGATGATCTGACCTCCTTG 624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 CTCAGTGCCCGGCTGGACCTCCAATGATCGTGGAGGAGATGAAG 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   506 TCATTAGCAATATCAGTTACACAGCCCACCACCTGCGGACGCTG-ACCAGCAATCTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 1.1e-20;
0; Mismatches 217; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                               Score 112.8; DB 1;
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPHONE: (517) 227-5941
INFORMATION FOR SEQ ID NO: 61:
                                                                                                                                                                                                                                                                                          6.7%;
                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 506 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                            Query Match 6.7%
Best Local Similarity 53.8°
Matches 254; Conservative
                                                                                                                                                                             single
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MEDIUM TYPE: Floppy
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CITY: San Francisco
                                                                                                                                      TYPE: nuclear sinc
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976 GGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCC 1035
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                                                                                                                                                               916 GAGAGAGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAA 975
                                                                                                                                                                                                                               856 ACTGGCAACAAGGGACAGAAAGGAGAAGGGGGGGGGGCCTGGACCACCTGGCCCTGCGCGGT
                                                                                                                                                                                                                                                                                                                                                   1036 AGTGGGGACCCCAGGCCCCCCGGGCCCACCAGAAAGAGGGACTCCCCGGCCCTCAGGGC
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                                          Length 1608;
                                                                                          0; Mismatches 205; Indels
                                               Score 106; DB 4;
Pred. No. 1.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08253155A
Patent No. 5691147
GENERAL INFORMATION:
APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
UNMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/253,155A FILING DATE: 02-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: LAHIVE & COCKFIELD 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: MII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEPAS: (617) 227-5941
INFORMATION FOR SEQ ID NO: 20:
                                               6.3%;
52.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                               Query Match 6.3
Best Local Similarity 52.8
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1216 CCTGGCCCATCAGG 1229
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CITY: Boston
STATE: MA
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US-08-253-155A-20
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  US-09-029-348-19
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DESCRIPTION OF ARTIFICIAL SEQUENCE: SEQUENCE
OTHER INFORMATION: DERIVED FROM CDNA OF PROCOLLAGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.3%; Score 106; DB 1; Length 432; Best Local Similarity 54.0%; Pred. No. 6.8e-19; Matches 217; Conservative 0; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1192 GGCCCCAAGGGCCCCCCCGGCCCTCCTGGCCCATCAGGAGCG 1233
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Patent No. 6171827
GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: 6087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
                                                                                   NAME: ROWLAND, BELLTAM I.

REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A5556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELERAX: (415) 494-8701
TELERAX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: US/08/642,255
                                                                                                                                                                                                                                                                                                                                                                         , molecule TYPE: other nucleic acid; DESCRIPTION: /desc = "synthetic" US-08-642-255-48
                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                          LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 20 SOFTWARE: Patentin Ver. 2.0
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                     FILING DATE:
CLASSIFICATION:
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LENGTH: 1608
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2380 AAATGGTGCTCCGGGGGAACAAGGCCTACAAGGATTAACAGGGCACAAAGGATTTCTTGG 2439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       852 CCCAACTGGCAACAAGGACAGAAAGGAGAGAAGAGGGGGGAGCCTGGACCACCTGGCCCTGC
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APPLICANT:
APPLICANT:
G.
TITLE OF INVENTION: Alpha---
TITLE OF INVENTION: Polynucleotides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Yale University, Office of Cooperative Research
""DREET: 246 Church Street
                                                                                                                                                                                                                                                                                                                                join(2..82, 86..97, 101..4399, 4403..4420, 4424
..4465, 4469..4876, 4880..5101)
                                                                                                                                                                                                                                                                                                                                                                                                              Score 100; DB 1; Length 5102;
Pred. No. 8.4e-17;
0; Mismatches 200; Indels
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Patent No. 542408
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T., Morrison, Karen E.,
APPLICANT: G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 800K storage
                      28,665
FR: 40397/104/BABR
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                                        REFERENCE/DOCKET UNMBER: 4039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 5.9%;
Best Local Similarity 52.4%;
Matches 220; Conservative
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OPERATING SYSTEM: Macinto
                                                                                                                                                                                             LENGTH: 5102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
      NAME: SAXE, Bernhard D. REGISTRATION NUMBER: 28
                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                          ; NAME/KEY:
; LOCATION:
; LOCATION:
US-08-494-168-1
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      567 AGTCAGGACCACTTGCACAGATACCCTTACCAAACACACAGATGATGATGTGTGACCTTGAA 626
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APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                       Length 503;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
                                                                                                                                                       6.2%; Score 105.4; DB 1; 52.9%; Pred. No. 1.1e-18;
                                                                                                                                                                         .1e-18;
                                                                                                                                                                               Pred. No. 1.1e
0; Mismatches
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08494168 Patent No. 5731192 GENERAL INFORMATION:
LENGTH: 503 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                 Conservative
                                                                                                                                                                           Local Similarity
ses 226; Conserv
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                                                                                      ; MOLECULE TYPE:
US-08-253-155A-20
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                                                                                                                                                       Query Match
                                                                                                                                                                             Best Loca
Matches
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Hudson, Billy

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RESULT 10
US-08-399-889-1
Sequence 1, Application US/0839989B
; Patent No. 5973120
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; LOCATION: (1)..(1416)
US-08-399-889-1
                                                                                                                                                                                                                                                                                                                           ORGANISM: Calf
                                                                                                                                                                                                                                                                                             LENGTH: 1416
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                                                                                                                                                                                                                                                                                                              TYPE: DNA
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                                               Query Match 5.9%; Score 99.6; DB 1; Best Local Similarity 51.6%; Pred. No. 5.9e-17; Matches 228; Conservative 0; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHROMOSOME/SEGMENT: NO. 5424408 known PUBLICATION INFORMATION: NO. 5424408e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         No. 5424408 known
SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/621,091G
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                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Calf
STRAIN: Unknown
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976 GGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCC 1035
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GENERAL INFORMATION:

APPLICANT: Reeders, Stephen T

APPLICANT: Reeders, Stephen T

APPLICANT: Hudson, Karen E

APPLICANT: Hudson, Rally G

TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides

TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides

CURRENT APPLICATION NUMBER: US/08/399,889B

CURRENT FILING DATE: 1995-03-07

EARLIER APPLICATION NUMBER: 07/621091

EARLIER FILING DATE: 1990-11-30

NUMBER OF SEQ ID NOS: 25

SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Reeders, Stephen T
APPLICANT: Morrison, Karen E
APPLICANT: Hudson, Billy G
TITLE OF INVENTON: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 9512638
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Patent No. 6007980
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Best Local Similarity 51.6<sup>†</sup>
Matches 228; Conservative
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Gaps

Length 1416

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976 GGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCC 1035
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a Collagenous Domain and the
Polypeptide Chain Encoded by
such a Sequence
                                               0; Mismatches 214; Indels
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Patent No. 5691197
GENERAL INFORMATION:
APPLICANT: Tryggvason, Karl
APPLICANT: Elomaa, Outi
APPLICANT: Kangas, Maarit
TITLE OF INVENTION: An Insolated DNA Sequence For Patent No. 5691197
      Score 99.6; DB 4;
Pred. No. 5.9e-17;
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STREET: 1100 Superior Avenue
STREET: Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,367B
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ATTORNEY/AGENT INFORMATION:
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                                             Matches 228; Conservative
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TITLE OF INVENTION: a CC
TITLE OF INVENTION: BOLI
TITLE OF INVENTION: SUCI
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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STATE: Ohio
      Query Match
Best Local Similarity
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US-08-392-367B-1
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Patent No. 6277558
GENERAL INFORMATION:
APPLICATION:
APPLICATION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 95-1263-C
CURRENT APPLICATION NUMBER: US/09/439,897
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                      Length 1416;
                                                                                                                                                                                                                                                                                                                                                           0; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                    Score 99.6; DB 3;
Pred. No. 5.9e-17;
CURRENT APPLICATION NUMBER: US/09/167,364
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 08/399889
EARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 1
LENGTH: 1416
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Best Local Similarity 51.6%;
Matches 228; Conservative
                                                                                                                                                                                                                                 ; NAME/KEY: CDS
; LOCATION: (1)..(1416)
US-09-167-364-1
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) LOCATION: (1)..(1416)
US-09-439-897-1
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ORGANISM: Bos taurus
FEATURE:
                                                                                                                                                                    TYPE: DNA
ORGANISM: Calf
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961 CCCATGGGGTCCCCTGGAGCTCAGGGAGGTAAAGGTGATGCTGGAAAACCAGGCCTACCA 1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.9%; Score 99.4; DB 3; 1
Best Local Similarity 51.5%; Pred. No. 7.6e-17;
Matches 229; Conservative 0; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:

NAME: Minnich, Richard J.

REGISTRATION NUMBER: 24,175

REFERENCE/DOCKET NUMBER: TRV 2 009

TELECOMMUNICATION INFORMATION:

TELEPHONE: (216) 861-5582

TELEX: (216) 241-166

TELEX: (216) 240-166

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Nucleotide-genomic DNA;
HYPOTHETICAL: No. 6063901 relevant
HYPOTHETICAL: No. 6063901 relevant
NOS-08-893-467A-1
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/893,467A
                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 720 Kb storable
COMPUTER: IBM PS/2, Model 35 SX
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                                                                                                                                                                                                                          Word Perfect 5.1
                                                                                                                                                                                                       DOS 5.0
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TYPE: Nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
  Suite 700
                                                                                                                                                                                COMPUTER: IBM PS/
OPERATING SYSTEM:
SOFTWARE: Word Pe
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                       Cleveland
                                                               X: U.S.A. 44114-2518
                                               Ohio
                       CITY: Cle
STATE: OF
COUNTRY:
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US-08-555-669-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                   Length 1868;
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a Collagenous Domain and the
Polypeptide Chain Encoded by
such a Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Trygyason, Karl
APPLICANT: Elomaa, Outi
APPLICANT: Elomaa, Outi
APPLICANT: Elomaa, Outi
APPLICANT: Arangas, Maarit
TITLE OF INVENTION: An Insolated DNA Sequence For a
TITLE OF INVENTION: No. 6063901el Macrophage Receptor
TITLE OF INVENTION: a Collagenous Domain and the
TITLE OF INVENTION: Such a Sequence
                                                                                                                                                                                                                                                                                                                                                                                 Score 99.4; DB 1;
Pred. No. 7.6e-17;
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                                                                                                                                                                                                                                                                  MOLECULE TYPE: Nucleotide-genomic DNA
HYPOTHETICAL: No. 5691197 relevant
HYPOTHETICAL: No. 5691197 relevant
MIT-SENSE: No. 5691197 relevant
              REFERENCE/DOCKET NUMBER: TRV 2 009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 241-166
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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24,175
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Best Local Similarity 51.5%;
Matches 229; Conservative (
                                                                                                                                                                         LENGTH: 1868 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
REGISTRATION NUMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    Linear
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Length 1868;

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Sequence 11, Application US/08555669
Patent No. 5773348
GENERAL INFORMATION:
APPLICANT: Brewton, Richard
APPLICANT: Mayne, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 99.4; DB 1; Length 2
Pred. No. 8.8e-17;
0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/555,669 FILING DATE: 13-NOV-1995 CLASSIFICATION: 435
                                                                                                                                                               ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFRENCE/DOCKET NUMBER: 8389-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3664
TELERAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.9%;
Best Local Similarity 51.5%;
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
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; LOCATION:
US-08-555-669-11
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944 CCGGGCATGCCAGGCAAGGACGGCCAGAATGGCGTGCCAGGACTCGATGGCCAGAAGGGA 1003
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1004 GAGGCTGGTCGCAACGGTGCTCCGG 1028 1213 CCTCCTGGCCCATCAGGAGCGGTGG 1237 δλ

Search completed: March 21, 2003, 08:25:28 Job time: 79.7466 secs

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DNA encoding novel
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Nucleotide sequenc
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Human COL5A3 CDNA
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/note= "fragment specifically claimed in claim
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55..1698
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/product- "collectin"
                                                                                                                                                                                                                                                                                                                                                                                                                AAH78667
AAQ43032
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AAD06573
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                                                                Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
low density lipoprotein; ss.
                                                                                                                                                                                                                                                                                                                                                                                  The present sequence encodes a human scavenger receptor, designated SRCL-P1. The SRCL-P1 polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic complications, bacterial infection and restenosis following angioplasty, which are associated with accumulation of exidized low density
                                                                                                                                                                                                                                                                                                                                     useful for treatment and diagnosis of diseases associated with oxidized low-density lipoprotein accumulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     ipoprotein and the binding of advanced glycation end-products into
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                                              Nucleotide sequence of a human scavenger receptor
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                                                                                                                                                    "scavenger receptor"
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; Pred. No. 0;
0; Mismatches
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                                                                                                                        Location/Qualifiers
74..2302
/*tag= a
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100.0%;
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2000JP-0309068
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                            (first entry)
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Matches 1355; Conservative
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                                                                                                        Homo sapiens
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10-OCT-2000;
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          AAH43036;
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, may cardial infarctions, thrombophiebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                        One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGCAACAAGATTTGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATT
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                                                                                                                                                                                                                                          Claim 1; Fig 27; 567pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 99.9
Matches 1349; Conservative
                      (PAON') PAONI N F.
(STEP/) STEPHAN J F.
(WATA-) WATANABE C K.
(WILL/) WILLIAMS P M.
(WOOD/) WOOD W I.
  MARSTERS S A.
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               PAN J.
PAONI
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                                                                                                                                                               Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary;
antiarteriosclerotic; gene; ss.
                                                                                                                                         Human angiogenesis related cDNA PRO7223 SEQ ID NO: 27.
 2594 TGGAACACTCCAATCAGAAAAGGTTATCATCCCG 2628
                                                              ВР
                                                             ABL95574 standard; cDNA; 2005
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2000US-220624P.
2000US-220664P.
2000WO-US20710.
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2000WO-US23328.
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2000WO-US30873,
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2001WO-US00000
                                                                                                                 (first entry)
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GODOWSKI P J.
GURNEY A L.
HILLAN K J.
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FERRARA N.
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25-JUL-2000;
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23-AUG-2000;
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24-OCT-2000;
26-NOV-2000;
20-DEC-2000;
20-DEC-2000;
21-SEP-2000;
23-AUG-2000;
24-OCT-2000;
26-NOV-2000;
26-PER-2001;
27-DEC-2000;
28-PER-2001;
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09-MAR-2001; 2
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10-MAY-2001; 2
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25-MAY-2001; 2
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28-JUN-2001;
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Gaps

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wound healing; chromosome mapping; gene mapping;
 Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; anglogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphanglits; tumour anglogenesis; breast carcinoma; liver carcinoma;
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TTGGGAACTAAAATGTTCCCCAGGGTGATATGCTGATTTTCATTGTGCACATGGACTGAA
                                                   TTTTCAGTTGAGAAAGTTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA
                                                                                  GATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGGTCAT
                                                                                                                                                                          GGCCATGGGCCAGGAGAAGACTGTGCTGGGTTTTATGCTGGGCAGTGGAACGATTTC
                                                                                                                                                                                                        CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCT
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                      GCACCGGAGGACAATGGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTAT
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or anglogenic disorder in a mammal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma and and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paon1 NF;
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Ye W;
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2000WO-US32678.
2000WO-US34956.
2001WS-0767609.
2001US-0796498.
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2001US-0854280
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2000US-222695P
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2001US-0808689
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Stephan JF, Watanabe CK,
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WO200200690-A2.
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25 MAY 2001;
25 MAY 2001;
25 MAY 2001;
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25-JUL-2000;
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02-AUG-2000;
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01-MAR-2001;
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28-FEB-2001;
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                            DB 24; Length 2005;
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gene mapping. ABL88259 to ABL88267 represent the exemplification of the present invention.
                                        1; Indels
                T; 0 other;
                           Score 1337.4;
Pred. No. 0;
0; Mismatches
                 415
                606 A; 493 C; 491 G;
                           Query Match 98.7%;
Best Local Similarity 99.9%;
Matches 1349; Conservative
                Sequence 2005 BP;
chromosome and
probes used in
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1438 CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACGGGGGGACAGTCATCTTT
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                                                                     CCAATTACTGAAAAAATTGACAGCTAGTGTTTTTTACCATCCGTCATTACCCAAAGAC
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Zhang J
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Yang Y,
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Wehrman T, Xt
Goodrich R,
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2000us-0552317.
2000us-059042.
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25-APR-2000; 2
09-JUL-2000; 2
19-JUL-2000; 2
03-AUG-2000; 2
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19-OCT-2000;
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Wang J, 1
Zhao QA,
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1323 TTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA 1382
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                                                                                                                                               immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polynucleotides are useful in gene therapy. A composition containing a polynucleotide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous and size of containing the neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C. N. S disorders.

Oct. S disorders.
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Extracellular matrix and adhesion-associated protein; EXMAD;
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                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-2, EXMAD-1, EXMAD-1, EXMAD-5, EXMAD-6, EXMAD-7, EXMAD-10, EXMAD-10, EXMAD-11, EXMAD-12, EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-17, EXMAD-17, EXMAD-17, EXMAD-17, EXMAD-19, EXMAD-20, EXMAD-21, EXMAD-23, EXMAD-27, E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 2641;
                                                                                                                                                                                 Isolated polynucleotide encoding extracellular matrix or adhesion-associated protein (EXMAD) useful for diagnosing, tre preventing disorders associated with expression of EXMAD such
                                               Baughn MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                               Yue
                                                                                                                                                                                                                                                      proliferative, immune and genetic disorders -
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  (INCY-) INCYTE GENOMICS
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Secreted protein; human; nutritional supplements; immune stimulant; immune suppressor; haematopoiesis requiator; itssue growth; chemotaxis; activin/inhibin; chemotinesis; haemostasis; thrombolysis; receptor/ligand activity; anti-inflammatory; tumour inhibitor;
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                                                                             CATCTTGTTTTCATAAACACTAGAGGGAACAGCAATGGATAAAAAAACAGATGGTAGGG
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                        TCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAG 360
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                                             TTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence encodes a human secreted protein of the invention.

This DNA sequence was isolated from a human adult brain cDNA

This DNA sequence was isolated from a human adult brain cDNA

This DNA sequence was isolated from a human adult brain cDNA

Ilbrary, and was designated clone bv2271. The DNAs and proteins

suitable for treating, preventing or ameliorating medical conditions in humans and animals. Although no supporting data is given. Suggested clivities include nutritional sources or supplements, immune stimulating or suppressing activity, heamatopolesis regulating activity, classing growth activity, anti-inflammatory activity, cadherin/tumour receptor/ligand activity, anti-inflammatory activity, and tumour inhibition activity. The DNAs are also stated to be useful for gene therapy, A host cell transfected with the DNA, or its subfragments and variants is useful for recombinant production of the human secreted protein clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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    derived from
ovary, adult

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCGGCTGAGAGAGGCCCAATTGGACCAGCTGGTCCCCCCGGAGAGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding secreted human proteins -
human foetal brain, adult brain, foetal kidney, adult
retina, adult placenta or adult uterus cDNA libraries
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Treacy M;
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Pred. No. 0;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 26; Page 87-88; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                   SH,
V,
                                                                                                                                                                                                                                                                                                                                                                                                     K, Howes Spaulding
                                                                                                                                     97US-0868696.
97US-0868698.
97US-0868898.
97US-0868899.
97US-0868890.
97US-0868900.
97US-0868900.
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99.8%;
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97US-0869194
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Best Local Similarity 99.8
Matches 1348; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     Fechtel
                                                                                                                                                                                                                                                                                                                                                                                                                         Racie LA,
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04-JUN-1997;
04-JUN-1997;
04-JUN-1997;
04-JUN-1997;
04-JUN-1997;
  WO9855614-A2
                                                                            01-JUN-1998;
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                                       10-DEC-1998
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                                                                                                                                                         04-JUN-1997
04-JUN-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                       McCoy
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM36642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the Activity the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                he sequence data for this patent did not form part of the printed
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                                                                                                                                                      Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; heemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel nucleic acids and polypeptides, useful for treating disorders
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Zhang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2181 BP; 664 A; 539 C; 535 G; 443 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang Y,
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Xu C, Xue AJ,
, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 4617; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                such as central nervous system injuries
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                                                                                                                          polynucleotide SEQ ID NO 4617
                             AAI60628 standard; cDNA; 2181 BP
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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2000US-0653450.
2000US-0662191.
2000US-0693036.
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2000US-0598042.
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                                                                                           (first entry)
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P-PSDB; AAM41472.
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                      leukaemia; ss
                                                                                                                                                                                                                                                                     Homo sapiens.
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29-NOV-2000;
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Zhao QA,
                                                            AA160628;
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           AAI60628
ID AAI6
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           GCGGGTGAGAGAGCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGCCGGCAAAGGA
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                                                                                     TCTAAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAG
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ATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATA
                                               CCTCGGGGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCCC
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                                                                           181 GCCCCAACTGGCAACAAGGACAGAAAGGAGAGAGAGGGGGGAGCCTGGACCACCTGGCCCT
                                                                                                                                                                                            361 GGCCCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGGACTCCCCGGCCCT
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Gaps

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7; Indels

DB 22; Length 2181;

Score 1328.8; Mismatches

98.18;

99.48;

Best Local Similarity 99.4 Matches 1344; Conservative

Query Match

Pred. No.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis
                                                                                      The invention relates to human secreted or transmembrane protein (I),
                        CCATTTACTGAAAAAATTGACAGCTAGGGTTTTTTACCATCCGTCATTACCCAAAGAC
                                                                        TTGGGAACTAAAATGTTCCCCAGGGTGATATGCTGATTTTCATTGTGCACATGACTGAA
                                                                                                                          TCACATAGATTCTCCTCCGTCAGTAACCGT-GCGATTATACAAATTATGTCTTCCAAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collins-Racie LA,
                                                                                                                                                                                         ATGGAACACTCCAATCAGAAAAAGGTTATCAT 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 250; Page 231-232; 284pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LaVallie ER,
Spaulding V;
                                                                                                                                                                                                                                                                                                                                        Human polynucleotide SEQ ID NO 69.
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                                                                                                                                                                                                                                                              ABQ92072 standard; cDNA; 2929
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MCCOY J M.
LAVALLIE E R.
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P-PSDB; ABP61859.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EVANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacobs K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TREA/) (SPAU/)
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their fragments and is encoded by specific complementary deoxyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or amaliorating a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cutokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activity relating to angiogenesis, cutokines. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace. (C cells damaged by illness, autoimmune disease, accidental damage or regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic activity, regulation of haematopolesis and is useful for treating myeloid call disorders, platelet disorders such as thrombocytopaenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoprosis, osteoarthritis, bone degenerative disorders or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rhemmatoid arthritis, disbections, autoimmune disorders e.g. multiple sclerosis, rhemmatoid arthritis, mystelmia gravis, allergic reactions and conditions, contractions and conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                     The
                                                                                                                                                                                                                                                                                                                   The invention relates to a human scavenger receptor-like protein. The protein is useful as a target molecule for diagnosis, prevention and treatment of autoimmune diseases such as rheumatoid arthritis.
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treatment of autoimmune disease, such as rheumatoid
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arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
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                                                                                                                                                                                           2194 CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCT 2253
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                                                                                              2134 GGCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTC
CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCT
                        TTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA
                                                      GATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGGTCAT
                                                                                                                                   2074 GAIGGGACAICICCAGACIACAAAATIGGAAAGCIGGACAGCCGGAIAACIGGGGICAI
                                                                                                                                                   GGCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTC
                                                                                                                                                                                                                                                                                                                       Nucleotide sequence of a human scavenger receptor.
                                                                                                                                                                                                                                                                                                                                                                                                              "scavenger receptor"
                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
92..2320
                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                               arteriosclerosis; diabetes;
low density lipoprotein; ss.
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2000JP-0309068,
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P-PSDB; AAG63347.
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The present sequence encodes a human scavenger receptor, designated SRCL-P1. The SRCL-P1 polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic complications, bacterial infection and restenosis following angioplasty, which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products into
                                                                                                                                                                                                                                                                                                                                                                        1471
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                                                                                                                                                                                         BP; 829 A; 617 C; 635 G; 556 T; 0 other;
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les 228;
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Pred. No. 9.5e-
0; Mismatches
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                                                                       CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCT 1020
                                                                               GCATTATAACGGACTGTGATGGGATCACATGAGCAAATTTTCA--GCTCTCAAAGGCAAA 1078
                                                                                                                                        AACCAATTACTGAAAAAAATTGACAGCTAGTGTTTTTTACCATCCGTCATTACCAAAG 1198
                                                                                                                                                                                                                                           GAATCACATAGATTCTCCTCCGTCAGTAACCGTGCGATTATACAAATTATGTCTTCCAAA 1317
                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                               ATATTATAACAGCATGATATAATAGCAGAAACATATTTCTGATGCCTCTGAAAGCCGAA
                                                                                                                                                  ACTIGGGAACTAAAATG-TICCCCAGGGTGATATGCTGATTTTCATTGTGCACATGGACT
                                                                                                                                                                                  GAATCGCATAGATTTTCTCAGCCATTAACCATAGAATTTATGCAAAGTATATCTTTCCAA
       GATGGGACATCTCCAGACTACAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCAT
                      GACGGGTCACCTGTTGATTACAAAACTGGAAAGCTGGACAACCAGATAACTGGGGCAGT
                                      GGCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #6937
                                                                                                                                                                                                                                                                           GTATGGAACACTCCAATCAGAAAAG 1343
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; ABG06946.
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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The invention relates to isolated polynucleotide (I) and probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of stres expressing (II). (I) and (II) are useful in medical imaging of stres expressing (II). (I) and (II) are useful in medical imaging of stres expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in casponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Contino acid sequences AAS64197-AAS94564 represent novel human but was obtained in electronic format directly from WIPO are the contino acid sequences and partent did not appear in the printed appear in the printed and product of the invention.
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99.8%; Pred. No. 6.7e
ive 0; Mismatches
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Length 2256;

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                                                                                                                                                                                                                                                                                    Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
low density lipoprotein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic complications, bacterial infection and restenosis following angloplasty, which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scavenger receptor proteins SRCL-P1 with collectin-like structure, ful for treatment and diagnosis of diseases associated with oxidized
                                                                                                         903
                                                                             951
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes a human scavenger receptor, designated SRCL-P1. The SRCL-P1 polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal
                                      891
 CATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTCCAA
                   GGGACATCTCCAGACTACAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGC
                                                                                                                                     TGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGT 1010
                                                                                                                                              Sequence 2256 BP; 721 A; 524 C; 528 G; 483 T; 0 other;
                                                                                                                                                                                                                                                                 Nucleotide sequence of a human scavenger receptor
                                                                                                                                                                                                                                                                                                                                                                          "scavenger receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         low-density lipoprotein accumulation
                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                        AAH43054 standard; DNA; 2256
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2000JP-0309068
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P-PSDB; AAG63350.
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                                                                       1393 ACTACAAGGTCCACGGGCCCCAGGGGTCCAAGAGGTGACAGGATCCCAGGGACCCCC 1452
                                                                                                                      1453 TGGCCCAACTGGCAACAAGGGACAGAAAGGAGAGAAGGGGGAAGCCTGGAC----CACCTGG 1509
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                                                                                                549 TGCCCCATCAGGAGCGGTGGTGCCCTGGCCCTGCAGAATGAGCCAACCCCGGCACCGGA
                                                                                                                                                                                                                                             849 ATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGCCATGG
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                        Indels
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                          Mismatches
  Score 743.8;
Pred. No. 1.6
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54.9%;
nilarity 91.9%;
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02-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-APR-2000;
07-JUL-2000;
07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JU
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14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAAAGCTGGAC-AGCCGGATAACT-GGGGTCATGGCCCATGGGCCAGGAGAAGACTGTGCT 927
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                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -
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                     DNA encoding novel human diagnostic protein #6935.
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                                                                                                                                                                                                                                                                                30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; imunosoppressive; antihifiammatory; anti-HHV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antializeric; antifilaleric; antilioler; anticonvulsant; antifingal; antipinal antiparastic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                                                                                                                                                                                                                                                                                                                             1227 GATATGCT-GATTTTCATTGTGCACATGGACTGAATCACATAGATTCTCCTCCGTCAGTA 1285
                                                                                                                                                      1048 CATGAGCAAATTTTCAGCTCTCAAAGGCAAAGGACACTCCTTTCTAATTGCATCACCTTC
                                                             253 CATGAGCAAATTTTCAGCTCTCAAAGGCAAAGGACACTCCTTTCTAATTGCATCACCTTC
                                                                                                                                                                                                                                                                                  133 AGTGTTTTTTACCATCCGTCATACCCAAAGACTTGGGAACTAAAATGTTCCCCAGGGGT
                                                                                                                           1108 TCATCAGATTGAAAAAAAAAAGCACTGAAAACCAATTACTGAAAAAAATTGACAGCT
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2000US-0190076.
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2000US-0231244.
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2000US-0230437.
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2000US-0235836.
2000US-0236327.
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune chaemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 3224 human nervous system antigen polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for preventing, diagnosing and/or treating nervous system cancers and metastases .
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Sequence 5041 BP; 1480 A; 1074 C; 1103 G; 1384 T; 0 other

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X65018 H.sapiens m

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BC022318 Homo sapi

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APO00122 Homo sapi
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-MODEL-frame+_p2n.model -DEV=xlp
-MODEL-frame+_p2n.model -DEV=xlp
-DG-cgn2_1/USPTO_spool/US09763712/runat_14032003_100949_18101/app_query.fasta_1.1877
-DB-cgn2_1/USPTO_spool/US09763712/runat_14032003_100949_18101/app_query.fasta_1.1877
-DB-GenEmbl -OFWH=fastap -SUFFIX-rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bits -MINMATCH=0.7 -ALIGN=200 - LIST=45
-OOGALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MINNO -ALIGN=15 -MODE=LOCAL
-OOGALIGN=200 -THR_SCORE=pct -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO_XLPXY -NO_MAPP -LAGREQUERY -NGS_SCORES=0 -WARIT -LONGLOG -DEV_TIMBOUT=120
-WARN_TIMBOUT=30 -THRRADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPDP=6 -FGAPEXT=7
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Ohtani,K.
Direct Submission
Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College,
Department of Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa,
Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:+81-166-68-2293, Fax:+81-166-68-2399)
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LEGVPGMPGPRGFQPGSGAVVPALALQNEPTPAPBDNGCPPHWKNTDCYTSYSVE
KEIFEDAKLFCEDASHLVFINTFEDQWIKKQMVGRESHWIGLTDSFRENEWKWLDG
TSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAAGQWNDFOCEDVNNFICEKDREHTVLS
           2983 bp mRNA linear PRI 21-NOV-2001 for collectin placenta 1, complete cds.
                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                              Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Keshi,H., Sakai,Y., Fukuoh,A., Sakamoto,T., Itabe,H., Suzutani,T., Ogasawara,M., Yoshida,I. and Wakamiya,N.
The membrane-type collectin CL-Pl is a scavenger receptor vascular endothelial cells
J. Biol. Chem. 276 (47), 44222-44228 (2001)
2 (bases 1 to 2983)
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="female"
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/gene="CL-P1"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 264)
Bandman,O., Hillman,J.L., Tang,Y.T., Lal,P., Yue,H., Baughn,M.R.,
Lu,D.A. and Azimzai,Y.
Extracellular matrix and adhesion-associated proteins
Patent: WO 0068380-A 39 16-NOV-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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AB038518 3058 bp mRNA linear PRI 08-MAR-2001 Homo sapiens SRCL mRNA for scavenger receptor with C-type lectin type I, complete cds.
AB038518 GI:13365514
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Nakamura,K., Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura,T.
Molecular cloning and functional characterization of a human scavenger receptor with C-type lectin (SRCL), a novel member of a scavenger receptor family
Biochem. Biophys. Res. Commun. 280 (4), 1028-1035 (2001)
2 (bases 1 to 3058)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical
Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical
School, Division of Biochemistry, Biomedical Research Center; 2-2
yamadaoka, Suita, Osaka 565-0871, Japan
(E-mall:knakamureconbich,med.osaka-u.ac.jp,
Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
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STNSELSTFRSDILDLRQQLREITEKTSKNKDTLEKLQASGDALVDRQSQLKETLENN
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Ohtani, K., Suzuki, Y., Eda, S., Kawai, T., Kase, T., Keshi, H., Sakai, Y., Fukuoh, A., Sakamoto, T., Itabe, H., Suzutani, T., Ogasawara, M., Yoshida, I. and Wakamiya, N. CDNA cloning of mouse CL-P1 gene
Unpublished
I to 2637)
Sakai, Y. Eukuoh, A., Sakamoto, T. and Wakamiya, N. Direct Submission
IL Submitted (18-JAN-2002) Katsuki Ohtani, Asahikawa Medical College, Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa, Hokkaido 078-8810, Japan (E-mail:Ohtaniesashikawa-med.ac.jp, Tel:81-166-68-2393, Fax:81-166-68-2399)
                                           Sciurognathi; Muridae; Murinae; Mus
                                    Craniata; Vertebrata; Euteleostomi;
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/db_xref="GI:21901969"
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/db_xref="taxon:10090"
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Nakamura,K. and Nakamura,T.
Nakamura,K. and Nakamura,T.
Nakamura,K. and Nakamura,T.
Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical School, Division of Biochemistry, Biomedical Research Center; 2-2 yamadaoka, Suita, Osaka 565-0871, Japan (F-mall:knakamur@onbich.med.osaka-u.ac.jp, Tel:81-6-6879-3788)ex. 3783, Fax:81-6-6879-3789)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus srcl mRNA for scavenger receptor with C-type lectin, complete cds.
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Homo sapiens SRCL mRNA for scavenger receptor with C-type lectin
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    (sites)
    Nakamura, K., Funakoshi, H., Miyamoto, K., Tokunaga, F. and Nakamura, T.

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GSRGSPGKPGPQGPSGDPGPPGFREGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPG
LPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTPAPEDNSKSKPSLQPGGQGSACA"
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                                                                                                                            Direct Submission
Submitted (04-DEC-2000) Kenji Nakamura, Osaka University Gradu
School of Medicine, Division of Biochemistry, Biomedical Resea
Center; 2-2 yamadaoka, Suita, Osaka 565-0871, Japan
(E-mail:knakamur(Goobich.med.osaka-u.ac.jp, Tel:81-6-6879-3783,
Pax:81-6-6879-3789)
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                                   scavenger receptor family
Blochem. Blophys. Res. Commun. 280 (4), 1028-1035 (2001)
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2 (bases 1 to 4330)
Nakamura,K. and Nakamura,T.
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Molecular cloning and functional characterization of a scavenger receptor with C-type lectin (SRCL), a novel scavenger receptor family
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                                               PheGlnLeuPheGluThrAspIleValAsnIleIleSerAsnIleSerTyrThrAlaHis
                                                                                                                                         ThrLysHisThrAspAspLeuThrSerLeuAsnAsnAshThrLeuAlaAsnIleArgLeuAsp
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0 410	QQ	2028 CCTTAGCCTCCCAGGTAGCTGGGAATACAAGCGTGTGCCCCCACAGCCAGC	
2088 TATTTTAGAGGGGTTTCACAGGGGGGGGGGGTGTTCAAACTGGGGGGTG 410	οy		
218 AAGTGATCCACCTACTATCCCAAAGTGCTGGGAATACGGTTGACCACCACTTGTTTTTTTT	QQ	TATTITIAGTAGAGGGGTTTCACAGTGTTGGGCAGGGTGGTTTCAAACTTCTGGCCTC	
2148 AAGTGATCCACCTACTACTTTCCCAAAGTGCTGGGAATACAGGTGTGAACCACCACGT 410  2268 CTGCTGCCAGAACAGGCCTCCATACTATTAACAGCATTGTGTCTCTCTC	δ		
410	q	AAGTGATCCACCTACCTAGTTTCCCAAAGTGCTGGGAATACAGGTGTGAACCACCACGTT	
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10	q	TTGTCCCCCGGCTGCATATTAACAGCAAAGGCATCATAGGGGGTTGGCACAGAGGC	
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1328 TTTAGTGCTCATTTGTTTTATGTATTAGTGTATGTATGGGACAGGGTCTACTGT 10  1248 CACCAGGCTGGAATGACGAAGTGAAGTGCAACATAGCTCATTGCAGCTTTGACCT 110  1248 CACCAGGCTGGAATGTTTTTTTTTTTTTTTTTTTTTTTT	λά		
410	q	TTTAGTGCTCATTTGTTTTATGTATTATGTGTGTATGGGACAGGGTCTCACTCTGT	-
2388 CACCCAGGCTGGAATGACGAAGTGAAGTGCAAACATAGCTCATTGACCT 410	λ̈́		-
410  2508 CACCACACCTGGCTAATTTTTTATTTTCCTTTTTGTAGAACCGGGACCAGGGGTATGC 410  2508 CACCACACCTGGCTAATTTTTTTTTTTTTTTTTTTTTTT	ą	CACCCAGGCTGGAATGACGAAGTGAAGTAGCAAACATAGCTCATTGCAGCTTTGACCT	
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2508 CACCACACCTGGCTAATTTTTATTTTCTTTTTTGTAGAAACAGGGTCTTGCTATGTTGC 410	λ̈		
410	q	CACCACACCTGGCTAATTTTTTATTTTCCTTTTTGTAGAAACAGGGTCTTGCTATGTTGC	
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410	q	CCAGGCTGGTCTTGAACTCCTGGCCTCAAGCAACCCTCCTGCCTCAGTCTTGCAAAGTGC	
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410	ą	16GGATTCCAGGTGGGAGCCACTGCACCTGGCTCTTGCATTTATATATA	
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410	ð	GCCCTCAGAAGACAAACACAATGCAAAACATTTCCTTCAGGGAAGCCTGCTGGCCGCCT	
2748 GAGCGCTCTTCCCTCGTTTTACATCCTCGGAGATAGATGGGCCTCCTCGGTTAGC 410	λ		
410	q	GAGCGCTCTTCCCTCGTTTTACATCCTCACTCTGGAGATAGAT	
2808 TCCATCAACATGTGGATGGAACCCTCTGCTATTGATGATTAATTTCTTTTTGAG 410	λy		
410	ą	TCCATCAACATGTGGATGGAACCCTCTGCTATTGATGACTACATTTAATTTCTTTTGAG	
2868 AAAGGTGTTAGATGTTACGGTGCCTTCTAGTCTTTTGATAATTAAAACTTTTGGCAAAACT 410	λλ		
410	ą	AAAGGTGTTAGATGTTACGGTGCCTTCTAGTCTTTTGATAATTAAACCTTTGGCAAAACT	
2928 CGAATGTTGGTTAGCAACCAAGCCTATTTTCTCTCTCTTTGACCCAACCGCTATTCTA 410	λy		
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2988 TIGATITIGGTCGGTGAGGCCCGGGTTATITIGTTGATCCGTGAGCCCATTITIGGTGC 410	λλ		
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SOS	ource 12005 /organism="Homo sapiens"	<b>q</b> a	   847 G	GGGGACC
BASE COUNT ORIGIN	/db_xrer="taxon:9606 606 a 493 c 491 g	Qy		ProGlyP
Alignmer Pred. NG Score: Percent	7.47e-86 Length: 2688.00 Matches: 99.60% Conservative:	do go	369 L	CCTGGCT
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	SerLeuGloffbrieger Grandon Grandon Franco Grandon Karlandon Karlan	QV	429 G      1147 G	GluLysg         GAGAAAG
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Qy 16 Db 36	169 LeuAsnGluValArgThrThrCysThrAspThrLeuThrLysHisThrAspAspLeuThr 188 	Qy Dp		Aspvala              GACGTCA
Oy 16 Db 45		RESU AX49 LOCU DEFI	RESULT 8 AX490920 LOCUS DEFINITION	AX490
Qy 20 Db 46	209 AspLeumetArgSerArgLeuAspThrGluValAlaAsnLeuSerVallleMetGluGlu 228 	ACCE VERS KEYW SOUR	ACCESSION VERSION KEYWORDS SOURCE	AX490 AX490
Qy 23	MetLysLeuValaspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGly	OR	ORGANISM	Homo Eukar Mamma
	ProbroG1yProArgG1yProArgG1ySprgG1ySerG1nG1yProProG1yProThr 	AU	AUTHORS	Baker Godow: Paoni
Oy 26 Db 66	269 GlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGlu 288 	IT. OU	TITLE JOURNAL	Compos disor Paten Genen
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Db 847 GGGGACCCAGGCCCCAGGCCCAGCAAAGAGGGACTCCCCGGCCCTCAGGCCCT 906	Qy 349 ProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGly 368	Db 907 ccrdccrrccaggacrrcaggcaccaccgrrcaggaaccrgcaggrccrcagaccrcagga 966	QY         369 LeuProGlyLeuProGlyValProGlyMetDroGlyProLysGlyProProGlyProPro 388           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 389 GlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrProAlaProGlu 408	Qy 409 AspasnGlyCysProProHisTrpLysAsnPheThrAspLysCysTyrTyrPheSerVal 428	Qy 429 GluLysGluIlePheGluAspAlaLysLeuPheCysGluAspLysSerSerHisLeuVal 448	Qy 449 PheIleasnThrargGluGluGluGlnTrpIleLysLysGlnMetValGlyArgGluSer 468 	Qy 469 HisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGlyThr 488	Qy 489 SerProAspTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGly 508	Qy 509 ProGlyGluAspCysAlaGlyLeuIleTyrAlaGlyGlnTrpAsnAspPheGlnCysGlu 528	Oy 529 AspValAsnAsnPheIleCysGluLysAspArgGluThrValLeuSerSerAlaLeu 547 	ESULT 8 490920 OCUS EFINITION CCESSION ERSION EXWORDS	SOURCE human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.	REFERENCE 1 AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Pani, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.	and 1e,W. TITLE Compositions and methods for the diagnosis and treatment of diagnosis and treatment of	JOURNAL Patent: WO 0200690-3 77 03-JAN-2002; Genentech, Inc. (US) FRANTIBES CLOST CONTROL OF CONTRO	rce	BASE COUNT 606 a 493 c 491 g 415 t
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Query Match:
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Genome Project.

This clone (DKF2p547G1215) is available at the RZPD in Berlin.
Plass clone (DKF2p547G1215) is available at the RZPD in Berlin.
Plasse contact the RZPD: Ressourcencescentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
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/clone_lib="547 (synonym: hfbr1). Vector pSport1; host
DH10B; sites NotI + SalI"
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CTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCAAGGGCCCCCCCGGCCCTCCT 1026
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo
Bumanalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1886)
Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERWANY
                                                                                                 PhelleAsnThrArgGluGluGlnGlnTrpIleLysLysGlnMetValGlyArgGluSer
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Mismatches:
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collangelo, M., Collins, S., Collymore, A., Cooke, P., Castlano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Peterson, K., Pollara, V., Riley, R., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
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1 (bases 1 to 169088)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone RP11-324G2
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                                                                                               GlyCysProProHisTrpLysAsnPheThrAspLysCysTyrTyrPheSerValGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                       843 GGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTATTTTCAGTTGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             903 GAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATTTTTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AsnThrArgGluGluGlnGlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1083 GACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGCCATGGGCCAGGA
                                                                        PheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGlyLeuPro
                                                                                                                                                                          GlyLeuProGlyValProGlyMetProGlyProLysGlyProProGlyProProGlyPro
                                                                                                                                                                                               GCTTGCCTGGGGTACCAGGCATGCCAGGCCCCAAGGCCCCCCCGGCCCTCTGGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlullePheGluAspAlaLysLeuPheCysGluAspLysSerSerHisLeuValPheIle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        471 IleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGlyThrSerPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AspTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169088 bp DNA linear Homo sapiens chromosome 18 clone RP11-324G2 map 18, SEQUENCE, 8 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC016128
AC016128.4 GI:10046526
HTG; HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens.
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misc_feature
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                                                                                                                                                                            BASE COUNT
ORIGIN
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№
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                                                            Center for Genome
                                                                                                                                                                                                                                                                   Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 324_G_2
Sequencing vector: M13; M77815; 108 of reads
Sequencing vector: M13; M77815; 1008 of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 167224 bases at least Q30
Consensus quality: 167296 bases at least Q30
Consensus quality: 167996 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 18388; sum-of-contigs
Quality coverage: 6.2 in Q20 bases; sum-of-contigs
Quality coverage: 6.5 in Q20 bases; sum-of-contigs
                        Direct Submission

Direct Submission

Submitted (20-NOV-1999) Whitehead Institute/MIT Center fo

Research, 320 Charles Street, Cambridge, MA 02141, USA

On Sep 9, 2000 this sequence version replaced gi:6649269.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
------- Project Information
Center project name: L999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1794 18043: contig of 17943 bp in length

1794 18043: gap of 100 bp

1804 22424: contig of 4381 bp in length

22425 2524: gap of 100 bp

38095 38194: gap of 100 bp

100 bp
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/clone_lib="RPC1-11 Human Male BAC"
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                              Center code: WIBR
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                        TITLE
JOURNAL
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                                                                                                                  COMMENT
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165612 ATGTATTCTCATAATGTGGTCATCATGAACCTCAACCTGAACCTGACCCGAGGTGCAG 165553
                                                                                                                                                                                                                                                                                                                                                                                                              165132 CACCTGCGGACGCTGACCAGCAATCTAAATGAAGTCAGGACCACTTGCACAGATACCCTT 165073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 165072 ACCAAACACACAGATGATCTGACCTCCTTGAATAATACCCTGGCCAACATCGGTTTGGAT 165013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HisLeuArgThrLeuThrSerAsnLeuAsnGluValArgThrThrCysThrAspThrLeu 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 GlnMetGluAsnIleThrThrIleSerGlnAlaAsnGluGlnAsnLeuLysAspLeuGln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    141 PheGlnLeuPheGluThrAspIleValAsnIleIleSerAsnIleSerTyrThrAlaHis 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerValSerLeuArgMetGlnGlnAspLeuMetArgSerArgLeuAspThrGluValAla 220
                                                                                                                                                                                                                                                                                           1 MetTyrSerHisAsnValValIleMetAsnLeuAsnAsnLeuAsnLeuThrGlnValGln 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 ThrLysHisThrAspAspLeuThrSerLeuAsnAsnThrLeuAlaAsnIleArgLeuAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 AlaLysAlaAsnAsnAspThrLeuGluAspMetAsnSerGlnLeuAsnSerPheThrGly
                                                                                            700 others
                                                                                                                                                                                     0000
                                                                                                                                                                                     Conservative:
Mismatches:
                                                                                            ų
                                                                                                                                                       Length:
Matches:
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/note="assembly_fragment"
120970. .169088
/note="assembly_fragment
                                                                                            52660
                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                           (1-169088)
                                                                                                                                                                                                                                 Gaps:
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                                                                           vector_side:right"
a 33537 c 34088 g
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                                                                                                                                                                                                                                                             US-09-763-712A-2 (1-547) x AC016128
                                                             clone_end:T7
                                                                                                                                                5.17e-34
1239.00
100.008
100.008
41.738
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Best Local Similarity:
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                                  misc_feature
                                                                                                                                        Alignment Scores:
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SOURCE

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consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
       This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133090 133189; gap or

133190 141206: contig of 8017 bp in length

141207 141306: gap of 100 bp

141307 141306: contig of 744 bp in length

149051 149150: gap of 100 bp

149151 156105: contig of 6955 bp in length

156106 1562048: contig of 6955 bp in length

156204 162148: gap of 100 bp

162149 162148: gap of 100 bp

165119 16518: contig of 2843 bp in length

165119 16518: contig of 2262 bp in length

165119 16518: contig of 2262 bp in length

165119 16518: contig of 2262 bp in length

16781 167880: gap of 100 bp

16781 16988: contig of 2406 bp in length

16987 17008; gap of 100 bp

170087 171909: contig of 103 bp in length

172318 17217: gap of 100 bp
                                                                                                                                                                                                                                                                                                                       65158: gap of 100 bp
81322: contig of 16164 bp in length
81422: gap of 100 bp
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24384 46875: contig of 22492 bp in length
                                                                                                                                                                                                                                                                              ap of 100 bp
contig of 18083 bp in length
                                                                                                                                                                                                                                                                                                                                                                          100 bp
f 17401 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                        p of 100 bp
contig of 11145 bp in length
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110169 122716: contig of 12548 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122717 122816: gap of 100 bp
122817 133089: contig of 10273 bp in length
                                                                                                                                                                                                    24283: contig of 24283 bp in length
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141307. .149050
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46976 65058; conti
65059 65158; gap of
65159 81322; conti
81323 81422; gap of
81323 81422; conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133090 133189: gap of
133190 141206: conti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                                        98824 98923: gap of 98924 110068: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110169. 12271\overline{6}
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                                                                                                                                                                                                                                        1 (Dases 1 to 17802)
1 (Dullshed Only in Database (1999)
1 (Dullshed Only in Database (1999)
2 (Dases 1 to 17802)
2 (Dases 1 to 17802)
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       HTG 30-MAY-2000
AP000900 178022 bp DNA linear HTG 30-MAY-200
Homo sapiens chromosome 18 clone RP11-683J11 map 18p11.3, WORKING
DRAFT SEQUENCE, 20 unordered pieces.
                                                                                                                                                                                                      Vertebrata; Euteleostomi;
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Center clone name: RP11-68311
Center clone name: RP11-68311
Sequencing vector: PCR products; 100% of reads
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 170357 bases at least 040
Consensus quality: 170357 bases at least 030
Consensus quality: 174322 bases at least 020
Insert size: 176122; sum-of-contigs
Quality coverage: 4.56x in 020 bases; sum-of-contigs
                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Tu
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Contact: hattori@gsc.riken.go.jp
------ Project Information
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Homo sapiens DNA, clone:RP11-683J11
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 187635)

8 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Homo sapiens 187,635 genomic DNA of 18p11.3

1. Published Only in DataBase (2000)

1. Chases 1 to 187635)

8 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

1. Direct Submission

1. Submitted (05-JAN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC);

1. Submitted (05-JAN-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC);

1. Submitted (05-JAN-2000) Masahira Hattori, The Institute of Physical Appan (E-mail:Hattori@gsc.riken.go.jp, Tel:81-42-778-9923),

1. Published (15-2778-9924)
                                                                                                                                                                                                                                                                                       AP001022 187635 bp DNA linear HTG 30-MAY-2000 HOMO sapiens chromosome 18 clone RP11-815L4 map 18p11.3, WORKING DRAFT SEQUENCE, 33 unordered pieces.
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                                    SerValSerLeuArgMetGlnGlnAspLeuMetArgSerArgLeuAspThrGluValAla 220
                                                                                               221 AsnLeuSerVallleMetGluGluMetLysLeuValAspSerLysHisGlyGlnLeuIle
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Quality coverage: 4.35x in Q20 bases; sum-of-contigs
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Web Site: http://hgp.gsc.riken.go.jp/
Contact: hattoriegsc.riken.go.jp/
Contact: hattoriegsc.riken.go.jp/
Conter project Information
Center project Information
Center project name: Humbrafil8
Center clone name: RP11-81514
Center clone name: RP11-81514
Center clone name: RP11-81524
Center clone name: RP19-81514
Center clone name: RP19-81514
Consembly program: PRR products; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 177020 bases at least Q40
Consensus quality: 177020 bases at least Q20
Consensus quality: 182105 bases at least Q20
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* NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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99610: gap of 100 bp
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87899. 99510
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107374. .113189
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/chromosome="18"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                MetTyrSerHisAsnValValIleMetAsnLeuAsnAsnLeuAsnLeuThrGlnValGln
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  Conservative:
Mismatches:
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapplens genomic DNA
Published Only in Database (1999)
E. 2 (bases 1 to 188439)
S. Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
L. Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi, Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattorigasc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-84-5503-9111, Fax:81-45-563-9170)
On Apr 26, 2002 this sequence version replaced gi:9188470.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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* NOTE: This is a 'working draft' sequence. It currently

* consists of 32 contigs. The true order of the pieces

* is not known and their order in this sequence record is
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51011 51110: gap of 100 bp
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148740 153086; contig of 4347 bp in length
153087 153186; gap of 100 bp
153187 156921; contig of 5735 bp in length
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59022 163174: contig of 4153 bp
53175 163774: gap of 100 bp
63275 167066: contig of 3792 bp
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On May 31, 2000_this sequence version replaced gi:6997751.
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Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fullyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 188,255 genomic DNA of 18pll.3
Published Only in DataBase (1999)
2 (bases 1 to 188255)
Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fullyama,A., Yada,T., Totoki,Y., Matanabe,H. and Sakaki,Y. Direct Submission
                                  Quality coverage: 4.41x in Q20 bases; sum-of-contigs
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-839023.
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DRAFT SEQUENCE, 32 unordered pieces
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91010
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in length in length

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AC114677 182029 bp DNA linear HTG 10-JUN-2002
Mus musculus clone RP24-213K19, WORKING DRAFT SEQUENCE, 10 ordered
pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 182029)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-213K19
                                                                                                                                                                                                                                                                                                                                                                                 102661 ATGTATTCTCATAATGTGGTCATCATGAACCTCAACACCTGAACCTGACCCAGGTGCA 102720
                                                                                                                                                                                              102840
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                                                                                                                                                                                                                                                             AspTrpLeuLysGluLysValGlnSerLeuGlnThrLeuAlaAlaAsnAsnSerAlaLeu
                                                                                                           MetTyrSerHisAsnValValIleMetAsnLeuAsnAsnLeuAsnLeuThrGlnValGln
                                                                                                                                                                            GlnArgAsnLeuIleThrAsnLeuGlnArgSerValAspAspThrSerGlnAlaIleGln
                                                                                                                                                                                                                                             41 ArgileLysAsnAspPheGlnAsnLeuGlnGlnValPheLeuGlnAlaLysLysAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheGlnLeuPheGluThrAspIleValAsnIleIleSerAsnIleSerTyrThrAlaHis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HisLeuArgThrLeuThrSerAsnLeuAsnGluValArgThrThrCysThrAspThrLeu
            --0
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AC114677.3 GI:21362159
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
        Mismatches:
Indels:
Gaps:
                                                                         (1-188255)
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        99.60%
40.82%
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          Best Local Similarity:
                        Query Match:
DB:
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KEYWORDS
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167067 167166: gap of 100 bp 167067 167120: contig of 2954 bp in length 170221 170220: gap of 100 bp 170221 172430: contig of 2210 bp in length 172431 172530: gap of 100 bp 172431 172530: contig of 100 bp 172539 175698: gap of 100 bp 177218; gap of 100 bp 178532 178631: gap of 100 bp 178532 178631: gap of 100 bp 178632 178631: gap of 100 bp 178632 178653: contig of 1107 bp in length 178632 178653: contig of 1107 bp in length 178638 181064: contig of 1107 bp in length 181065 181164: gap of 100 bp 181065 181164: gap of 100 bp 18324 184022: gap of 100 bp 18334 184022: gap of 100 bp 18334 185310: gap of 100 bp 185311 187465 188255: contig of 1235 bp in length 187246 188255: contig of 1010 bp 11 length. Location/Cualifiers
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Matches:
Conservative:
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75157. 84737
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84818. 90909
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91010. 98615
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16197 . 33789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /map="18p11.3"
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1212.00
99.60%
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* NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the configs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* 1 951 contig of 951 bp in length

* 952 1051: gap of 100 bp

* 3807 3906: gap of 100 bp

* 3807 3906: contig of 2755 bp in length

* 3807 3006: contig of 4803 bp in length
                          Quality coverage: 8.0 in Q20 bases; agarose-fp
Quality coverage: 8.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                         8710 8809: gap of 100 bp
8810 17263: contig of 8454 bp in length
17264 17363: gap of 100 bp
17364 73638: contig of 19575 bp in length
3639 53226: contig of 16188 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69573 69672: gap of 100 bp
69673 89021: contig of 19349 bp in length
89022 89121: gap of 100 bp
89122 128310: contig of 39189 bp in length
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128411 182029: contig of 53619 bp in length.
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         Insert size: 181129; sum-of-contigs
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1052. .3806
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                Special to 182029)

Special to 182029,

Anderson. S., Barna, N., Bastlen, V., Bloom, T., Bogguslavkly, L.,

Boukhqalter, B., Brown, A., Camarata, J., Campoplano, A., Chang, J.,

Cook, A., Cooke, P., DeArtellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Faro, S., Ferreira, P., FitzHugh, M., Grand-Plerre, N.,

Rano, S., Gord, S., Goyette, M., Graham, L., Grand-Plerre, N.,

Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

Kamat, A., Karatas, A., Hulme, W., Iliev, I., Johnson, R., Jones, C.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,

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Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,

Oliver, J., Peterson, R., Phunkhang, P., Pierre, N., Pollara, V.,

Raymond, C., Rette, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,

Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R.,

Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,

Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,

Lalnoun, J., Zembek, L., Zimmer, A. and Zody, M.,

Direct Subnission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..... Genome Center
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Length: Matches:

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C (bases 1 to 2983)
Ohtani,K.
Direct Submission
Birect Submission
Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College,
Department of Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa,
Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:+81-166-68-2393, Fax:+81-166-68-2399)
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Oy Db 24	1 GTCACGAATCTGCAGCAAGATACCAGCGTGCTCCTCAGGGCAATCTGCAGAACCAAATGTAT 60 243 GTCACGAATCTGCAGCAACATACCAGCGTGCTCCAGCAATCTACAAATGTAT 302	qq	1323 CCCGGCCCTC
		Qγ	1141 GTGCCTGGAC
	01 ILICATARA TGTGGTCATCATGAACAACAACAACATGAACCAGGTGCAGGAAAACA IZU	qq	1383 GTGCCTGGAC
0y 13	121 AACCTCATCACGAATCTGCAGCGGTCTGTGGATGACAAGCCAGGCTATCCAGCGAATC 180	δλ	1201 GGCCCCCCCG
Dp 36		đ	1443 GGCCCCCCCG
Qy 16	181 AAGAACGACTTTCAAAATCTGCAGCAGGTTTTTCTTCAAGCCAAGAAGGACACGGATTGG 240	δŏ	1261 CCAACCCCGG
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Homo sapiens SRCL mRNA for scavenger receptor with C-type lectin
AP038518
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Nakamura,K., Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura,T.
Molecular cloning and functional characterization of a human
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TSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDFQCEDVNNFICEKDRETVLSS
                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura, K. and Nakamura, T.
Direct Submission
Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical
School, Division of Biochemistry, Biomedical Research Center; 2-2
yamadadow, Suita, Osaka 565-0871, Japan
(E-mail:knakamuréonbich.med.osaka-u.ac.jp,
Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                            TGGGGTCATGGCCATGGGCCAGGAGAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGG 1620
                                                        scavenger receptor with C-type lectin (SRCL), a novel member scavenger receptor family
Blochem. Biophys. Res. Commun. 280 (4), 1028-1035 (2001)
                      AAGTGGCTGGATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAAC
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/db_xref="taxon:9606"
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Williams, P. Mickey (US); Wood,
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  Hillan, Kenneth J. (US);
; Paoni, Nicholas F. (US)
Watanabe, Colin K. (US);
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Patent: WO 0208284-A 27 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
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Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
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CTGGCTTCCAGGGACTTCAGGCACCGTTGGGAGCCTGGGGTGCCTGGACCTCGGGGAC
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AX490920 2005 bp Sequence 27 from Patent WO0200690. AX490920 AX490920.1 GI:22323797
Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Jaker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Pan,I.K., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W
and re,W.  Compositions and methods for the diagnosis and treatment disorders involving angiogenesis  Patent: WO 0200690-A 27 03-JAN-2002;  Genentech, Inc. (US)  Location/Qualifiers
/organism="Homo sapiens" /db_xref="taxon:9606" / 493 c 491 g 4.
87.2%; Score 1477.6; 99.7%; Pred: No. 0; ive 0; Mismatches

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Ohtani, K., Suzuki, Y., Eda, S., Kawai, T., Kase, T., Keshi, H.,
Sakat, Y., Fukuoh, A., Sakamoto, T. and Wakamiya, N.
Direct Submission
Submitted (18-JAN-2002) Katsuki Ohtani, Asahikawa Medical College,
Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa, Hokkaido
078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:81-166-68-2393, Fax:81-166-68-2399)
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ACAATGGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTATTTTTCAGTTG
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                                                                                                                                                                                                             Length
                                                                                                                                                                                                             DB 10;
                                                                                                                                                                                                                               Pred. No. 9e-310;
0; Mismatches 210;
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87.6%;
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/ protein_id="BAB8249".1"
// protein_id="BAB8249.1"
// protein_id="BAB8249".1"
// protein_id="BAB8249"
Molecular cloning of a mouse scavenger receptor with C-type lectin (SRCL)(1), a novel member of the scavenger receptor family Biochin. Biophys. Acta 1522 (1), 53-58 (2001) 2 (bases 1 to 3291)
                                                                                          Nakamura, K. and Nakamura, T.
Direct Submission

Bundited (18 FEB-2000) Kenji Nakamura, Osaka University Medical
School, Division of Biochemistry, Blomedical Research Center; 2-2

Spandadoka, Sulta, Osaka 565-0871, Japan

(E-mail: knakamur@onbich.med.osaka-u.ac.ip,
Tel:81-6-6879-3783(ex.:3783), Fax:81-6-6879-3789)
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Pred. No. 1.3e-308;
0; Mismatches 213;
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/db_xref="taxon:10090"
1. .3291
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/product="scavenger
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Best Local Similarity 87.4%;
Matches 1482; Conservative
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Mus musculus srcl mRNA for scavenger receptor with C-type lectin,
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                        GGCAAAGGATCTAAAGGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCC
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SINSELSTERSDILDLRQQLREITEKTSKNKDTLEKLQASGDALVDRGSQLKETLENN
SFLITTVNKTLQAY ONGYVTULQQDTSVLQGHLONOMYSHNVYTMNLNNLINLLNLTDRNY
LITNLQRSVDDTSQAIQRIKNDFQUPSVLQGHKKDTDMLKEKVQSLQTLAANNSALA
KANDYLEDBNSQLNSFTGQMENITTSQANEBULKDLQDLHKOAENFRAIKFNQLEE
REQLEFIDIVNIISTAHHLRTITSNLASVTGTTGTTLTHTANTLANI
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LPGVPGMPGPKGPPGPPGPSGAVVPLALQNEPTPAPEDNSKSKPSLQPGGGGSACA"
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Nakamura,K., Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura,T.
Nakaeular Cloning and functional characterization of a human
scavenger receptor with C-type lectin (SRCL), a novel member of a
Biochem. Biophys. Res. Commun. 280 (4), 1028-1035 (2001)
2 (bases 1 to 4330)
Nakamura,K. and Nakamura,T.
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/product="scavenger receptor with C-type lectin type II"
/protein_id="BAB39148.1"
/db_xref="GI:13365553"
                                                                                                                                                                                                                                                                                                                                                                                                                                  4330 bp mRNA linear PRI 08-MAR-20
Homo sapiens SRCL mRNA for scavenger receptor with C-type lectin
type II, complete cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (04-DEC-2000) Kenji Nakamura, Osaka University Gradu
School of Medicine, Division of Biochemistry, Biomedical Resea
Center; 2-2 yamadaoka, suita, Osaka 565-0871, Japan
(E-mail:knakamur@onbich.med.osaka-u.ac.jp, Tel:81-6-6879-3783,
                                                                                          Length 4330;
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Pred. No. 2.2e-291;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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This clone (DKFZp547G1215) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSM802985 1886 bp mRNA linear PRI 20-MAR-2002
Homo sapiens mRNA; cDNA DKF2p547G1215 (from clone DKF2p547G1215).
AL713657
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Catarrhini; Hominidae; Homo.
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Enkaryorata; Devardata; Craniata; Vertebrata; Enteleostomi; Devaryora; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1886)
S Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
L Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GREMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email S.wiemann@dkfz-heidelberg.de; Sequenced by BMFZ (Blomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing conscritum of the Germa Genome Project.
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                       GTGCCTGGACCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCAAG
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/clone="DKRPp547G1215"
/tissue_type="brain"
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/gene="DKFZp547G1215"
/hote="similarity to a
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Center code: WIBR
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AC016128/c
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                                                                  Score 1251.4; DB 9;
Pred. No. 2.1e-284;
0; Mismatches 1;
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/gene="DKFZp547G1215"
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Unpublished

2 (bases 1 to 169088)

8 Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Bousely, Kiy, L., Boukhgalter, B., Barren, B., Linton, E., Bousely, R., Collins, S., Collymore, A., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Brachan, C., Dowar, K., Dowar, K., Dowar, K., Dowar, K., Dowar, K., Dowalan, L., Bardond, A., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKern, K., McLaughlin, J., Maldrim, J., McEwan, P., McGurk, N., Kiley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassliev, H., Vo, A., Wheeler, J., Wu, X., Direct Submission 1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Nill repeats were identified using RepeatWasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatWasker:html
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Birren, B., Linton, L., Musbaum, C. and Lander, E. Homo sapiens chromosome 18, clone RP11-324G2
                                                                                                                                          1522
                                                                                                                                                                                                             1080
                                                                                                                                                                                                                                                                                       1582
                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
GGATCGGCCTCACAGACTCAGAGCGTGAAATGAATGGAAGTGGCTGGATGGGACATCTC
                                                                                                                                                                       1021 GGATCGGCCTCACAGACTCAGAGCGTGAAATGAATGGAAGTGGCTGGATGGGACATCTC
                                                                                                                                                                                                                                                                                       1523 CAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGCCATGGGCCAG
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Center clone name: 324_G_2
Sequencing vector: M13: M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 165522 bases at least Q40
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 178022)

1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

1 Lobished Only in DataBase (1999)

2 (bases 1 to 178022)

1 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

1 Direct Submission

2 Lobished (17-Dec-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG 30-MAY-2000
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                             DD 165366 GCCAACAACGACCACCCTGGAGGATATGAACAGCCAGCTCAACTCATTCACAGGTCAGATG 165307
                                                                                                                                                                                                                                                                                                                                                                                                      165306 GAGAACATCACCACTATCTCTCAAGCCAACGAGAGAACCTGGAAGACCTGCAGGACTTA 165247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165126 CGGACGCTGACCAGCAATCTAAATGAAGTCAGGACCACTTGCACAGATACCCTTACCAAA 165067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 165066 CACACAGATGATCTGACCTCCTTGAATAATACCCTGGCCAACATCCGTTTGGATTCTGTT 165007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DD 164946 TCAGTGATTATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAAT 164887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           541 CGGACGCTGACCAGCAATCTAAATGAAGTCAGGACCACTTGCACAGATACCCTTACCAAA 600
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    121 AACCTCATCACGAATCTGCAGCGGTCTGTGGATGACAAAGCCAGGCTATCCAGCGAATC 180
                                                                                                                                                                                          241 CTGAAGGAGAAAGTGCAGAGCTTGCAGACGCTGGCTGCCAACAACTCTGCGTTGGCCAAA 300
                                                                                                                                                                                                                                                                                     301 GCCAACAACGACACCCTGGAGGATATGAACAGCCAGCTCAACTCATTCACAGGTCAGATG 360
                                                                                                                                                                                                                                                                                                                                                                                361 GAGAACATCACCACTATCTCTCAAGCCAACGAGCAGAACCTGAAAGACCTGCAGGACTTA 420
                                                                                               181 AAGAACGACTTTCAAAATCTGCAGCAGGTTTTTTTTAAAGCCAAGAAGGACACGGATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCTTTGAGACGGATATTGTGAACATCATTAGCAATATCAGTTACACAGCCCACCTG
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HOMO sapiens DNA, clone:RP11-683J11.
HOMO sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 167248 bases at least Q30 Consensus quality: 167996 bases at least Q20 Insert size: 177000; agarose-fp Insert size: 168388; sum-of-contigs Quality coverage: 6.2 in Q20 bases; sum-of-contigs Quality coverage: 6.5 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 169088;
                                                                                                                                                                                                                                                                                                                                                                 17944 18643: gap of 100 bp 18644 22424: contig of 4381 bp in length 22425 22524: gap of 100 bp 22525 38694: contig of 4381 bp in length 22525 38694: contig of 100 bp 38195 49220: contig of 100 bp 49321 49320: contig of 100 bp 49321 49320: gap of 100 bp 66395 66494: gap of 100 bp 66495 91692: contig of 25198 bp in length 91693 91792: gap of 100 bp 66495 91692: contig of 25198 bp in length 120870 120869: gap of 100 bp 120860: contig of 29077 bp in length 120870 120869: contig of 48119 bp in length.
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                                                                                                                                                                                                                                                                                                                                                          17943: contig of 17943 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
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100.0%; Pred. No. 3.8e-177;
Live 0; Mismatches 0;
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             133089: contig of 10273 bp in length
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                                     133090 133189; gap of 100 bp
133190 141206; contig of 8017 bp in length
141207 141306; gap of 100 bp
141307 149050; contig of 7744 bp in length
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174764 176271: contig of 1508 bp in length
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Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://ngp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924) On Mail 142-778-9940 On Mail 21, 2000 this sequence version replaced gi:6997403.
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                                                                                                                                                                                                                                                                                                                Sequencing vector: PCR products; 100% of reads chemistry: Dye-terminator Er-amersham; 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 161944 bases at least 040 consensus quality: 170357 bases at least 030 consensus quality: 174322 bases at least 020 misert size: 176122; sum-of-contigs Quality coverage: 4.56x in 020 bases; sum-of-contigs
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24384 46875; contig of 22492 bp in length
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65058: contig of 18083 bp in length
65158: gap of 100 bp
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81322: contig of 16164 bp in length
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                                                   Homo sapiens chromosome 18 clone RP11-815L4 map 18p11.3, WORKING DRAFT SEQUENCE, 33 unordered pieces. AP001022 GI:8117692
                                                                                        13764 TCTCTCAGGATGCAACAAGATTTGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTA 13823
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                                                                               TCTCATAATGTGGTCATCATGAACCTCAACAACCTGAACCTGACCCAGGTGCAGGAGG 120
                                                                                                                      AACCTCATCACGAATCTGCAGCGGTCTGTGGATGACAAGCCAGGCTATCCAGCGAATC 180
                                                                                                                                                                                                     CTGAAGGAGAAAGTGCAGAGCTTGCAGACGCTGGCTGCCAACAACTCTGCGTTGGCCAAA 300
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                       Gaps
                                         GTCACGAATCTGCAGCAAGATACCAGCGTGCTCCAGGGCAATCTGCAGAACCAAATGTAT
                                                                                                                                                             AAGAACGACTTTCAAAATCTGCAGCAGGTTTTTCTTCAAGCCAAGAAGGACACGGATTGG
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Length 178022;
                    Indels
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           Pred. No. 3.8e-177;
  DB 2;
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      100.0%; Pred. ....
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HOMO Sapiens DNA, clone:RP11-815L4.
Homo sapiens
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NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary; Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                    Physical
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 187635)
Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Published Only in DataBase (2000)
                                                                       Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
Submitted (05-JAM-2000) Masahira Hattori, The Institute of Phys and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail-hattori@gsc.riken.go.jp, URL:http://App.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924
                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will be
                                                                                                                                                         On May 31, 2000 this sequence version replaced gi:6997772
                                                                                                                                                                                                                                                                                                       Insert size: 184435; sum-of-contigs
Quality coverage: 4.35x in Q20 bases; sum-of-contigs
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force="assembly_fragment clone_end:T7 vector_side:right"
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 184842 184941: gap of 100 bp
184942 186345: contig of 1404 bp in length
186346 1845: gap of 100 bp
186446 187635: contig of 1190 bp in length.
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100.0%; Pred. No. 3.8e-177;
iive 0; Mismatches 0;
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126569, 131619_fragment"
/note="assembly_fragment"
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21433. .42072
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42173. .54336
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14433. .148902
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149003. .152918
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153019. .156399
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/db_xref="taxon:9606"
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Matches 798; Conservative
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182996 184841 contig of 1846 bp in length
184942 186345 contig of 1404 bp in length
186446 187635 contig of 1190 bp in length
Sequence updated (26-May-2000)
* NOTE: This is a "working draft' sequence. It currently
* consists of 33 contigs. The true order of the pleces
* is not known and their order in this sequence record is
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42173 54336: contig of 12164 bp in length
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66766: contig of 12330 bp in length
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107273: contig of 7663 bp in length
7373: gap of 100 bp
113189: contig of 5816 bp in length
3289: gap of 100 bp
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182896 182995; gap of 100 bp
182996 184841: contig of 1846 bp in length
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156500 158933; contig of 24
158934 159033; gap of 10
159034 101884; contig of 24
161885 161984; gap of 10
161985 164301; contig of 23
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131619: contig of
131719: gap of
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139925: contig of
0025: gap of
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182895: contig of
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148902: contig of
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176095: contig of
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177890: contig of
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179786: contig of
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181478: contig of
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Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Hono sapiens genomic DNA

L bublished Only in Database (1999)

E 2 (bases 1 to 188439)

E 3 (bases 1 to 188439)

E 4 Hattori,M., Ishil,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

L Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-Chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriggsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)

On Apr 26, 2002 this sequence version replaced gi:9188470.
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Homo sapiens genomic DNA, chromosome 18p clone:RP11-720L2, complete
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Length 188439;

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Score 798;

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Query Match

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AP000939 188255 bp DNA linear HTG 30-MAY-2000 Homo sapiens chromosome 18 clone RP11-839023 map 18p11.3, WORKING DRAFT SEQUENCE, 32 unordered pieces.
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Homo sapiens DNA, clone:RP11-839023.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                NOTE: This is a 'working draft' sequence. It currentl consists of 32 contigs. The true order of the pleces is not known and their order in this sequence record
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                                                                                                                                                                                                         Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp,
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Hattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 188,255 genomic DNA of 18p11.3
Published Only in DataBase (1999)
2 (bases 1 to 188255)
2 (bases 1 to 188255)
Pattori,M., Ishli,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                        May 31, 2000 this sequence version replaced gi:6997751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 171668 bases at least Q40 Consensus quality: 178865 bases at least Q30 Consensus quality: 18445 bases at least Q20 Insert size: 185155; sum-of-contigs
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                                                                                                                                                                                                                                                                                        URL:http://hpp.gsc.riken.go.jp,
URL:http://hpp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Pax:81-42-778-9924)
On May 31, 2000 this sommer
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------ Summary Statistics
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                                                                                                                                                                                                                                                                                                                                                                                             Center: RIKEN Genomic Sciences Center(GSC)
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Contact: hattori@gsc.riken.go.jp
------ Project Information
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Web site: http://hg
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Surren, B., Linton, L., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boquslavkiy, L., Anderson, S., Barna, N., Camenata, J., Campoplano, A., Chang, J., Chagaro, B., Cook, A., Cooke, D., Dekrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, A., Cooke, P., Pitzhano, K., Dewar, K., Diaz, J.S., Dodge, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., MacCann, C., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Olono, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Petterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Saman, S., Severy, P., Spencer, B., Stanger-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (10-MaR-2002) Whitehead Institute/MIT Center for Genome
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Db 103326 TCAGTGATTATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCACCATCAAGAAT 103385
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
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Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 182029)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Erown, A., Camarata, J., Campoplano, A., Chang, J.,
Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., Fitzeferald, M., FitzHugh, W., Gage, D.,
Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L.,
Johnson, R., Jones, C., Macdonald, P., Major, J., Marquis, N.,
Ilu, G., MacChan, C., Macdonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., MacDwan, P., McKernan, K., Lindblad-Toh, K.,
Liu, G., MacChan, C., MacGonald, P., Major, J., Marquis, N.,
Matthews, C., McCarthy, M., MacDwan, P., McKernan, K., Melain, J.,
Matthews, C., McCarthy, M., MacDwan, P., McKernan, K., Meldrin, J.,
Micol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P.,
O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S.,
Schupback, R., Seaman, S., Severti, M., Travis, N., Trigilio, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission

AL Submitted (10-JUN-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 10, 2002 this sequence version replaced gi:21328559.
All repeats were identified using Repeatwasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: 213_K_19

Sequencing vector: Plasmid; numery Statistics
Sequencing vector: Plasmid; numery Statistics
Chemiatry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 179506 bases at least 030
Consensus quality: 180723 bases at least 030
Consensus quality: 180723 bases at least 030
Consensus quality: 180700 bases at least 030
Consensus quality: 180700 bases at least 030
Consensus guality: 180700 bases at least 030
Consensus (B1129; sum-of-contigs
Quality coverage: 8.0 in 020 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: sequence_submissions@genome.wi.mit.edu
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69572: contig of 16246 bp in length
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17263: contig of 8454 bp in length
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JOURNAL
                                           REFERENCE
                                                                    AUTHORS
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COMMENT

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1931 GTCACAAATCTGCAACAAGATACTAGTGTGCTCCAGGGCAATCTGCAGAGCCAAATGTAT 1872
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 CTCTTTGAGACGGATATTGTGAACATCATTAGCAATATCAGTTACACAGCCCACCACCTG 540
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69573 69672: gap of 100 bp
69673 89021: contig of 19349 bp in length
89022 89121: gap of 100 bp
89122 128310: contig of 39189 bp in length
18311 128410: gap of 100 bp
128411 182029: contig of 53619 bp in length.
Location/Qualifiers
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1. .951
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3907. 8709
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8810. 17263
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17364. 36938
700te="assembly_fragment"
37039. 53226
70ote="assembly_fragment"
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a 37484 c 36555 g 52844
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/db_xref="taxon:10090"
/clone="RP24-213K19"
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Search completed: March 21, 2003, 06:24:31 Job time: 5262.67 secs

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Merberg, David
Treacy, Maurice
Spaulding, Vikki
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: CURRING DATE: 18-COMPUTED
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jacobs, Kenneth
MCGOY, John M.
LaVallie, Edward R.
Collins-Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 198, Application US/09745763 Patent No. US20020065394A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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STATE: MA
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                                         Sequence 57, Appl. Sequence 57, Appl. Sequence 4, Appl. Sequence 42, Appl. Sequence 206, App. Sequence 20, App. Sequence 21, Appl. Sequence 25, App. Sequence 766, App. Sequence 767, App. Sequence 768, App. Sequence 768, App. Sequence 768, App. Sequence 768, App. Sequence 762, App. Sequence 762, App. Sequence 762, App. Sequence 764, App. Sequence 104, Ap
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Sequence 782, App
Sequence 3946, Ap
                                                                                                                         March 21, 2003, 01:57:56 ; Search time 258.28 Seconds
   (without alignments)
   5089.177 Million cell updates/sec
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// cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
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// cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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version 5.1.4_p5_4578 - 2003 Compugen Ltd.
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US-09-924-340-57

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US-09-925-302-64

US-09-925-302-64

US-09-925-302-64

US-09-925-299-206

US-09-954-299-206

US-10-044-090-22

US-09-954-455-765

US-09-954-456-762

US-09-914-456-762

US-09-914-456-762
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Maximum Match 100%
Listing first 45 summaries
                                                                                      nucleic search, using sw model
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GenCore
Copyright (c) 1993
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length: 2000000000
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Maximum DB seq
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Perfect score:
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ENCODING THEM

Evans, Chery

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Sequence 725, App
Sequence 448, Appl
Sequence 368, Appl
Sequence 3685, Appl
Sequence 246, App
Sequence 613, App
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US-09-978-613

US-09-978-192A-613

US-10-175-737-331

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US-10-175-731

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US-10-176-913-331

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US-10-174-572-331

US-10-174-572-331
                      US-10-001-835-98
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                                                       Score 1681.4;
Pred. No. 0;
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                            NO: 198
       TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID
STRANDEDNESS: double
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Best Local Similarity 99.9%;
Matches 1693; Conservative
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US-09-745-763-198
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Sequence 782, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Sets
FILE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT FILIMG DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25

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ORGANISM: Homo sapiens
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Patent No. USZ0020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Useph G.
APPLICANT: Scherf, Useph G.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer; FILE REFERENCE: 44921-5028-W0.
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/217,054
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53.0%; Pred. No. 1.2e-19;
tive 0; Mismatches 210;
GCCCTCCTGGCCCATCAGGAGCGGTGG 1237
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Matches 237; Conservative
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APPLICANT: Fanaka, Hiroaki
TITLEOF ENVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REPERENCE: 91.052.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/293,574
                                                                                                                                                                                           ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z74615
US-09-880-107-3946
                                                                                                                                                                                                                                                                                                         Length 6728;
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3946
LENGTH: 6728
                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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; NAME/KEY: polyA_site
; LOCATION: 1118..1133
US-09-992-600A-57
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                                                                                                       LENGTH: 1133
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US-09-925-302-64
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APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.034.DIV
CURRENT APPLICATION NUMBER: 05/09/992,600A
CURRENT FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 08/9924,340
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR RELING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
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Matches 267; Conservative
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                                                                                                                                   NAME/KEY: polya_site
LOCATION: 1118..1133
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US-09-992-600A-57
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Pred. No. 5.6e-20;
0; Mismatches 229;
PRIOR APPLICATION NUMBER: US 60/299,698
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-05-25
SOFTWARE: JPatent
SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1230 AGCGGTGGTGCCCTGGCCTGCAG 1254
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Patent No. US20020044941A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.5%;
52.9%;
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Best Local Similarity 52.99
Matches 267; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 965.1133
FEATURE:
NAME/KEY: POlyA_signal
LOCATION: 1101.1106
FEATURE:
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2001-08-10

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CURRENT FILING DATE:
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US-09-880-107-3947
                                                                                                                                                                                                                                                                            LENGTH: 2192
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                                                                                                                                                                                                                                         SEQ ID NO 42
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Best Local Similarity 54.4%; Pred. No. 2e-19;
Matches 240; Conservative 1; Mismatches 197; Indels 3;
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO4
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILIKO DATE: 2001-08-10
PRIOR PILICATION NUMBER: PCT/US00/05918
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR PLICATION NOWER: 00/12
SOFTWARR: Petentin Ver. 2.0
SEQ ID NO 64
LENGTH: 2691
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
FEATURE:
NAME/FURS:
NAME/FURS:
NOTHER INFORMATION: n equals a,t,g, or c
NAME/FURS:
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NOTHER INFORMATION: n equals a,t,g, or c
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; Sequence 42, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
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GGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCC 1035
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                                                                                                                                                                                                                                                                                                                   Length 2192
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Patent No. US20020142981A1

GENERAL INFORMATION:

APPLICANT: HORDAY

APPLICANT: HORDE

APPLICANT: Scherf, Uwe

APPLICANT: Scherf, Uwe

TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;

FILE REFERENCE: 44921-5028-WO

CURRENT APPLICANTION NUMBER: US/09/880,107

CURRENT APPLICATION NUMBER: US 60/211,379

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-10-05

NUMBER OF SEQ ID NOS: 3950

SOFTWARE: PATENTIN VUMBER: US 60/237,054

PRIOR FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                Score 107.2; DB 10; Length
Pred. No. 7e-19;
0; Mismatches 228; Indels
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PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEO ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                   6.3%;
                                                                                                                                                                                                                                                                                                                   Query Match 6.3
Best Local Similarity 53.5
Matches 274; Conservative
                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                            OTHER INFORMATION: Genbank Accession No. US20020142981A1 274616
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| Publication No. US20030040617A9
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
| FILE REFERENCE: PAIO2
| CURRENT APPLICATION NUMBER: US/09/925,299
| CURRENT FILING DATE: 2001-08-10
| PRIOR APPLICATION NUMBER: ECT/US00/05883
| PRIOR FILING DATE: 2000-03-08
| PRIOR PILING DATE: 12099-03-12
| PRIOR FILING DATE: 1399-03-12
| SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                       Query Match 6.3%; Score 107; DB 10; Length 5 Best Local Similarity 51.3%; Pred. No. 1.3e-18; Matches 248; Conservative 0; Mismatches 235; Indels
                                                                                                         NAME/KEY: unsure
LOCATION: (1). (5086)
OTHER INFORMATION: n = a or c or g or t
                                                   ORGANISM: Homo sapiens
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LENGTH: 5145
SEQ ID NO 3947
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                                      TYPE: DNA
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Fatent No. US200200552741
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 206
LENGTH: 5145
                                                                                                                                                                                                                                                                                                                                             Length 5145;
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6.3%; Score 107; DB 9;
Best Local Similarity 51.3%; Pred. No. 1.3e-18;
Matches 248; Conservative 0; Mismatches 235.
                                                                                                                                                                                                                    NAME/KEY: misc_feature

) LOCATION: (5143)

) OTHER INFORMATION: n equals a,t,g, or c

01S-03-925-299-206
                                                                                          LOCATION: (17)

OTHER INFORMATION: n equals a,t,g, or NAME/FRY: misc_feature
LOCATION: (5126)

OTHER INFORMATION: n equals a,t,g, or
                                                 or
                    LOCATION: (4)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
misc_feature
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ORGANISM: Homo sapiens
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Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL: Program
SEQ ID NO 22
LENGTH: 5432
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Best Local Similarity 51.3%; Pred. No. 1.3e-18;
Matches 248; Conservative 0; Mismatches 235;
                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (4)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (17)
LOCATION: (17)
LOCATION: (17)
LOCATION: (17)
LOCATION: (5126)
                                                                                                                                                                                                                                      ; OTHER INFORMATION: n equals a,t,g, or c US-09-925-299-206
             ORGANISM: Homo sapiens
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APPLICANT: Recipon, Herve
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and
CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/259,563
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
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                                                                                                                                         Length 5432;
; FEATURE:
; NAME/KEX: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.13
US-10-044-090-22
                                                                                                                                         Score 107; DB 12;
Pred. No. 1.3e-18;
0; Mismatches 235;
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                                                                                                                                         6.3%;
                                                                                                                                                                                                 Matches 248; Conservative
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APPLICANT: Salceda, Susana
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CORGANISM: Homo sapien
US-10-001-887-33
                                                                                                                                                Query Match
Best Local Similarity
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Sequence 255, Application US/09964824A
Patent No. US20020102531A1
GENERAL INFORMATION:
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
TITLE OF INVENTION: Sets
FILE REPERENCE: 669290-73
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236,033
PRIOR FILING DATE: 2000-09-28
                                                                                                                                                                                                                                                                                                                                                                                                          962 GCAAAGGATCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCG 1021
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                                         TTACAATACTACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGG 841
                                                                                 837 TCACAGGCCCGAAAGGAGCAACGGGCCCCCCCAGGCATCAACGGCAAGGATGGGACCCCAG 896
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  0; Mismatches 215; Indels
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SOFTWARE: PatentIn version 3.0
  Matches 235; Conservative
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LENGTH: 2542
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Fatent No. US20020165180A1

GENERAL INFORMATION:

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc

TITLE OF INVENTION: Gene Sets

FILE REPERENCE: 68290-77

CURRENT APPLICATION NUMBER: US/60/233,133

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

WUMBER OF SEQ ID NOS: 1392

SOSTWARE: PatentIn version 3.0
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                                                               Gaps
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                                                             Indels
                   Score 106.8; DB 9;
Pred. No. 1.4e-18;
0; Mismatches 222;
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Pred. No. 1.6e-18;
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                 Query Match 6.3%;
Best Local Similarity 52.9%;
Matches 256; Conservative
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US-09-954-531-961
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Best Local Similarity
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US-09-954-531-961
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                                           TGCGGGTGAGAGAGCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGCGGCAAAGG
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
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1077 GGCCTCGAGGAAAATGGTCCCCAGGGCATCATGGGACAGAAGGGTGACCAAGGCGAGA 1136
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                                                                                                                                        1022 GCCCTCAGGCCCCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGACTCC 1081
                                                                                                                                                                                                                     1082 CCGGCCCTCAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGG 1141
                                                                                                                                                                                                                                                             1137 GGGGTCCAGTGGGGCAACCAGGCCTTCAGGGAAGGCAGGGCCCTAAGGGGGGAGCAGGGCC 1196
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PRIOR PILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR PAPLICATION NUMBER: US/60/235,840
PRIOR PILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
SOFTWARE: PATCHIN VONES: 2276
SOFTWARE: PATCHIN VERSION 3.0
SEQ ID NO 786
LENGTH: 5416
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PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
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PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
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Patent No. US20020115057A1
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hes 247; Conservative
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US:09-954-456-786
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AL568743 AL568743
BE910803 601661855
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BE290299 601089246
BF856923 QV1-F7024
BB248064 BB248064 BB248064
BM676508 UI-E-EJO-BQ771366 UI-M-FIO-24
AL543000 AL543000
AA361740 EST71069
AW379436 CM4-H7024
AL543000 AL543000
AA361740 EST71069
BC9128013 RC3-GN004
BI051416 RC5-GN028
BF854324 MR2-EN009
BE9228913 RC3-GN004
BI051416 RC5-GN028
BF85420 MR2-EN009
BG912097 CM4-GN036
BF856801 QV1-F7020
BE922978 RC3-GN004
AW240221 UP30b07.y
AL541116 AL542672
B1010883 MR2-EN009
BF854408 MR2-EN009
BF854408 MR2-EN009
BF854408 MR2-EN009
BF80004176 UI-H-EIO-BQ087163 AGENCOURT
BM721855 UI-S-E00-BI010883 MR2-EN009
BM907108 AGENCOURT
BM721861 W2444f06 x
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Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 1.0
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COMMENT
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AUTHORS
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                                                         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humpl
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                             Direct Submission
Submitted (05-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                  Sequencing Center
Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus, Similar to scavenger receptor with C-type lectin, clone IMAGE:2811487, mRNA.
                                                                                                                                                                                                                                                                                                                             Strausberg, R
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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Human Genome

Robin Humphreys

HTC 07-AUG-2002

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BASE COUNT
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         CACACAGATGATCTGACCTCCTTGAATAATACCCTGGCCAACATCCGTTTGGATTCTGTT
                                                                                                  GAGAACATCACCACTATCTCTCAAGCCAACGAGCAGAACCTGAAAGACCTGCAGGACTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:2811487"
/tissue_type="Mammary tumor.
old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pCMV-SPORT6"
757 c 760 g 757 t
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Pred. No. 0;
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5', mRNA sequence.
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EST.
house mouse.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Biosclence Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri
1 (bases 1 to 957)
11 (bases 1 to 957)
11 MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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Tissue Procurement: Susan L. Sullivan, PhD.
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/clone="IMAGE:6313500"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
note="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
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a 269 c 258 g 169 t 1 others
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
Unpublished (1999)
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5', mRNA sequence
BQ891432
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High quality sequence stop: 632
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie,
                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally
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/clone="IMAGE:6332754"
/clone_lib="NIH_MGC_130"
                                  /lab_host="DH10B (phage-resistant)"
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Tissue Procurement: Mark Maconoch
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National Institutes of Health, Mammalian
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BQ934501
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/clone="IMAGE:6330794"
/clone="Ib="NIH_MGC_130"
/clone="D="NIH_MGC_130"
/clone="OHIOB (phage-resistant)"
/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is
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                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11636 row: b column: 17
High quality sequence stop: 730.
                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                     Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                quality sequence stop:
Location/Qualifiers
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
                                    /clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross
/dev_stage="7 months"
/lab_host="DH10B"
                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:5251888"
                                                                                                            /organism="Mus musculus"
/strain="C57BL/6J"
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Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13721 row: n column: 01
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National Institutes of Health, Mammalian Gene
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/clone="IMAGE:6306240"
/clone="NIH_MCC_129"
/clone_lib="NIH_MCC_129"
/clone_lib="NIH_MCC_129"
/clone_lib="NIH_MCC_129"
/clone_"Third (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cl
unidirectionally. Primer: Oligo dT. Average insert
2.2 kb. Constructed by ResGen, Invitrogen Corp. Not
is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1988)
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Plate: LLCM2377 row: c column:
High quality sequence stop: 656.
Location/Qualifiers
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Tissue Procurement: ATCC
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Contact: Robert Strausberg,
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
          /tissue_type="epidermoid carcinoma, cell line"
/lab_host="DHIOB (phage-resistant)"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAGG). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

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                                                                                                                                                                                                                                      /clone_lib="NIH_MGC_102"
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                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 511)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                        BF805750 511 bp mRN
QV1-CI0173-071100-464-c02 CI0173 Homo
BF805750
BF805750.1 GI:12134739
EST.
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the Project. This entry can be seen in
                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                     Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 and
                                                                                                                                   Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF
                                                                                                                                                                              sequence tags
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FAPESP/LICR Human the following URL
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sapiens cDNA,
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SOURCE
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                                                                                                                                                                                                                                                                                                                                     CAACGAGCAGAACCTGAAAGACCTGCAGGACTTACACAAAGATGCAGAGAATAGAACAGC
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                                                                       B0127513 581 bp
ii60h06;yl Melton Normalized Mixed
musculus cDNA clone IMAGE:5946107 5
CSR2.; mRNA sequence.
B0127513
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Mus musculus
Eukaryota; M
                                                            BQ127513.1
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                              house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="CI0173"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev_stage="Adult"
 Metazoa; Chordata; Craniata; Vertebrata;
                                                              GI:20201424
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98.4%;
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Pred. No. 4.7e-109;
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                                                                                                       mRNA linear EST 19-APR-2002
d Mouse Pancreas 1 N1-MMS1 Mus
5' similar to TR:Q9UM15 Q9UM15
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Best Local Similarity
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                                                                                                                               146 CTGTGGATGACACAAGCCAGGCTATCCAGCGAATCAAGAACGACTTTCAAAATCTGCAGC
                                                   206
                                                                                                       61
                                                                                                                                                                                                                                         86 TCAACAACCTGAACCTGACCCAGGTGCAGCAGAGGAACCTCATCACGAATCTGCAGCGGT 145
                                                                                                                                                                                                           1 TCAACAACCTGTACCTACCCCAGGTTCAGCAGAGGAACCTTATCTCAAATCTGCAGCAGT
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                                                AGGTTTTTCTTCAAGCCAAGAAGGACACGGATTGGCTGAAGGAGAAAGTGCAGAGCTTGC
AGGTTTTCCTTCAAGCCAAGAAGGACACCGATTGGCTAAAGGAAAAAGTACAGAGCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing l
Washington University Genome Sequencing Center This clone is
available royalty-free through LLNL; please contact the IMAGE
consortium (info@image.llnl.gov) for further information
Seq primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi In
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
MA 02138
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Other_ESTs: ii60h06.x1
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                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreas, newborn pancreas, adult pancreas, and adult islets of Langerhans were separately constructed using SuperScript Plasmid Library kit (Life Technologies). CDNA was made by oligo-dT priming and size-selected by column fractionation. Libraries were amplified once on solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite chromatography and used to make this library."
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/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:5946107"
/clone_lib="Melton Normalized Mixed Mouse Pancreas
/clone_lib="Melton Normalized Mixed Mouse Pancreas
N1-MMS1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pSPORT1; Site_1: Not I; Site_2: Sal I; F
libraries representing EI0.5/12.5 pancreatic bud, E16.5
pancreas, newborn pancreas, adult pancreas, and adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              adult islet"
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Query Match Best Local 9 Matches 504;

Similarity

28.0%; 96.7%;

Score 475.4; DB 9; Pred. No. 1.1e-105; Mismatches

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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               222
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Location/Qualifiers
       /note="organ: placenta; Vector: pcMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcWVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email : filang@lifetech.com URL : thtp://fulllength.invitrogen.com"
                                                                                                                                                                                                                            /clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                /clone="CS0DE005YH04"
                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   BE910803 580 bp mRNA linear EST 29-SEP-2000 601661855F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3962292 5',
                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc
cDNA Library Arrayed by: The I.M.A.G.E. Consortion
                                                                                                               http://image.llnl.gov
Plate: LLAM9128 row: m column:
High quality sequence stop: 580.
                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL
                                                                                                                                                                     DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
                                                                                                                                                                                                                                                                                                   nmalia; Eutheria; (bases 1 to 580)
                       /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3962292"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
                                                                             /organism="Mus musculus
                                                                                                       Location/Qualifiers
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             Assessment of gene expression patterns metastasis using a 19,200 element cDNA Unpublished (2000) Contact: John Quackenbush
                                                                                                                                                                                             AW958053 STATES AW958053 AW958053
                                                                          1 (bases 1 to 552)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R.,
,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J.
                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                          Homo sapiens
                                                               Quackenbush,J.
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GI:8147736

2 bp MAGE

Homo mRNA

sapiens cDNA,

linear

mRNA sequence.

for Genomic

Research

microarray in a model

of,

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Local Similarity
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                                                                       AATGCTACTATTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAG
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GGAAGTGGCTAGACGGGTCACCTGTTGATTACAAAAACTG
                                                                                                              AGATGGTAGGGAGAGAGCCACTGGATCGGCCTCACAGACTCAGAGCGTGAAAATGAAT
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
a 153 c 161 g 107 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut.
Mammalia; Eutharia; Rodentia; Sciurognathi; Muridae; Mu.
E 1 (bases 1 to 601)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: ogapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hur
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTGGCCCTGCAGAATGAGCCAACCCCGGCACCGGAGGACAATGGCTGCCCGCCTCACTGG
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BE290299
BE290299.1 GI:
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Email: johnq@tigr.org
Plate: 115
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/db_xref="taxon:9606"
/db_cref="MAGE resequences, N
/clone_lib="MAGE resequences, N
/note="Vector: pBluescriptSKm"
112 c 143 g 121 t
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                                                                                                                                                                                                                                                                    ATCAGGAGCGGTGGTGCCCCTGGCCCTGCAGAATGAGCCAACCCCGGCACCGGAGGACAA 1283
                                                                                                                                                                                                                                                                                                                                   AGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCAAGGGCCCCCCCGGCCCTCCTGGCCC
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                                                                 AAACTCAAGAGAAGAACAGCCAATGGGTAAAAAAGCATACGTGGGGAGAGA
                                                                                               AAACACTAGAGAGGAACAGCAATGGATAAAAAAAACAGATGGTAGGGAGAGA 1454
                                                                                                                              AGAAA-TTTTGAAGATGCTAAGCTTTTCTGTGAAGACAAATCTTCCCCATCTCGTTTTCAT
                                                                                                                                             AGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCAT
                                                                                                                                                                                         CGGATGTCCGCCTCACTGGAAGAACTTCACAGATAAATGCTACTATTTTTCATTGGAAAA
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
plate: LLAM8516 row: k column: 12
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Location/Qualifiers
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/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtm12.pl?tl=QVI&t2=QV1-FT0201-021100-453-e01&t3=2000-11-02&t4=1)
Seq.primer: puc 18 forward
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Simpson A.J.G.
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/dev_stage="Adult"
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/db_xref="taxon:9606"
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URL:http://genome.gsc.riken.go.jp/

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
                                                                                                                                                                                                                                                                                                                                                                                                                                                Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizaw,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                           Hayashizaki,Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with

Computational Analysis of Full-Length Mouse cDNAs Compared with
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                                                                                                                                                                                          cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Grou
Genomic Sciences Center and Genome Science Laboratory in
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RIKEN integrated sequence analysis (RISA) system--384-format RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome 10 (11), 1757-1771 (2000)
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Muramatsu,M. and Hayashizaki,Y.
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/organism="Mus musculus"
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/dev_stage="7 days neonate"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
/note="Site_1
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/clone_lib="RIKEN full-length enriched, 7 days neonate
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Search completed: March 21, Job time: 2240.7 secs

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BASE COUNT ORIGIN

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11492.169 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result No. c 0 0 0 0 000 o o 1251.4 1086.2 1083 960.4 488.8 488.8 484.6 122.6 Score Match 1 1 4330 7 188439 7 188439 7 188235 5 1876322 5 1876325 7 188255 7 188255 7 1882029 3 1920029 3 1932029 3 1932029 3 1932029 3 1932029 2 3636 2 Length 1886 2637 DB 10 10 10 10 10 10 PALCOLIA AF137861 AF13883 AB008374 AB052836 AB007830 E32510 MMU16789 AF233390 AC025192 AC013643 AF235104 AR013643 AF235104 AR013643 AF235104 AR013668 AP000939 AC114677 AC102618 AC1124618 AC1124618 AC112418 AC112511 E32509 BC026446 AP000020 AP001022 AB009993 AX454442 AX490920 HSM802985 ) AB078434 AB038519 AB052103 AC016128 AP000915 AC024368 AP000900 AP001022 AP000939 AC126444 AC125058 H ALIGNMENTS AB007829 Homo sapi E32511 Scavenger r E32509 Scavenger r BC026446 Mus muscu AP000900 Homo sapi AP001022 Homo sapi AB00993 Mus muscu AC126444 Mus muscu AC125058 Mus muscu M25282 P.11vidus a AF278661 Rattus no AF13883 Bos tauru AB008374 Oncorhync AB052836 Oncorhync AX047353 Sequence AX047353 Sequence AB038518 Homo sapi AX454442 Sequence AX490920 Sequence AL713657 Homo sapi AB078437 Mus muscu AB052103 Homo sapi AC016128 Homo sapi AP000915 Homo sapi AP000915 Homo sapi AP000916 Homo sapi AP000929 Homo sapi AP000939 Homo sapi U16789 Mus músculu AF233390 Homo sapi AC025192 Homo sapi AC013643 Homo sapi AF235104 Homo sapi AF014116 Sequence AB008683 Bos tauru AB007830 Homo sapi E32510 Scavenger r Description E07265 cDNA encodi

RESULT 1
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LOCUS
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DEFINITION
AB005145
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ORGANISM
Homo sapiens female tissue\_lib:placenta cDNA to mRNA.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
REFERENCE
AUTHORS
Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Keshi,H.,
Sakai,Y., Fukuoh,A., Sakamoto,T., Itabe,H., Suzutani,T.,
Ogasawara,M., Yoshida,I. and Wakamiya,N.

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            ATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATTATGGAAGAAATGAAG
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ATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATTATGGAAGAAATGAAG
                                                     AATAATACCCTGGCCAACATCCGTTTGGATTCTGTTTCTCTCAGGATGCAACAAGATTTG
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J. Biol.
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2 (bases
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Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College,
Department of Microbiology, 2-1-1-1 Midorigaoka-Higashi, Asahikawa
Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:+81-166-68-2393, Fax:+81-166-68-2399)
                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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GSRGSPGKPGPOGPSGDPGPPGPFGERGPGGLPGTGGERGERGLPG
LPGVPGMPGPRGPGPGPGASAVVPLALQNBETPAPEDNGCPPHWKNETDKCYYFSVE
KEIFEDAKLFCEDKSSHLVFINTREEQQWIKKOMVGRESHWIGLTDSERENEWKWLDG
TSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDFQCEDVNNFICEKDRETVLSS
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/codon_start=1
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/db_xref="taxon:9606"
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KEYWORDS

AX047353 Sequence AX047353 AX047353.1

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                                                                                                                                                                                                                                                                                      Homo
                                       School, Division of Biochemistry, Biomedical Research yamadaka, Suita, Osaka 565-0871, Japan (E-mail:knakamur@onbioh.med.osaka-u.ac.jp, Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
                                                                                           2 (bases 1 to 3058)
Nakamura, T.
Nakamura, T.
Direct Submission
Submitted (18-FEB-2000) Kenji Nakamura,
                                                                                                                                                   Biochem. Biophys. Res. 21092718
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Mammalia; Eutheria; Primates; Catarrhini;
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/product="scavenger receptor with C-type lectin type I"
/protein_id="BAB39147.1"
/db_xref="c1:13365515"
/translation="MKDDFAEEEEEVQSFGYKRFGIQEGTQCTKCKNNWALKFSIILLY
ILCALLTITVAILGYKYVEKMDNVTGGMETSRQTYDDKLTAVESDLKKLGDQTGKKAI
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                                                                                                                                                                                              Sequence
AX454442
Compositions and methods for the diagnosis disorders involving angiogenesis Patent: WO 0208284-A 27 31-JAN-2002; Genentech, Inc. (US); Baker, Kevin P. (US); Gerber, Hanspeter (US); Gerritsen,
                                                             and
                                                                      Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                 TTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGACCTCGGGGACTGCCA
                                                        CCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAAGGCTCCCAG
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                                                                                                          GGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCCAGTGGGGAC
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GGCTTGCCTGGGGTACCAGGCCAGGCCCCAAGGGCCCCCCCGGCCCTCCTGGCCCA
                                                                                                 GGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCCAGTGGGGAC
                                                                                                                                       CCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAAGGCTCCCAG
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/db_xref="taxon:9606"
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                                       ATGAACAGCCAGCTCAACTCACTCACAGGTCAGATGGAGAACATCACCACTATCTCTCAA
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Sequence 27
AX490920
AX490920.1
                                                                                                                                                                                                                           Compositions and methods for the diagnosis disorders involving angiogenesis Patent: WO 0200690-A 27 03-JAN-2002;
                                                                                                                                                                                                                                                                           Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J. Paonl,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.
                                                                                                                                                                                                                   Genentech, Inc. (US)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/db_xref="taxon:9606"
493 c 491 g 41
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                      ATCGGCCTCACAGACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTCCA
                                                                                                                                               AGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTATTTTTCAGTTGAGAAA
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AL713657.1 G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Ca
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charit
Berlin/Germany) within the cDNA sequencing consortium of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This clone (DKF2p547G1215) is available at the RZPD in Please contact the RZPD: Ressourcenzentrum, Heubnerweg Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de Fl
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Submitted (12-MAR-2002) MIPS,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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/clone_lib="547 (synonym: h
DH10B; sites NotI + SalI"
/dev_stage="fetal"
  ρ
                                                                                                                                                                           /translation="AikfnQLEERFQLFETDIVNIISNISYTAHHLRTLTSNLNEVRT
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NDFQCEDVNNFICEKDRETVLSSAL"
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/db_xref="GI:19584340"
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/note="similarity to
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/db_xref="taxon:9606"
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Mus musculus (
AB078434
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Submitted (18-JAN-2002) Katsuki Ohtani, Asahikawa Medical College,
Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa, Hokkaido
078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:81-166-68-2393, Fax:81-166-68-2399)
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Ohtani, K., Suzuki, Y.,
Sakai, Y., Fukuoh, A.,
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Ogasawara,M.,
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i,Y., Fukuoh,A., Sakamoto,T., Itabe,H.,
awara,M., Yoshida,I. and Wakamiya,N.
cloning of mouse CL-P1 gene
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KFTFETDAKLFGFMKSGILVETNGFFFGNKKKKGFFFFASEVNGCFFFFTBKCTYFFSLE
                                                 KEIFEDAKLFCEDKSSHLVFINSREEQQWIKKHTVGRESHWIGLTDSEQESEWKWLDG
SPVDYKNWKAGQPDNWGSGHGPGEDCAGLIYAGQWNDFQCDEINNFICEKEREAVPSS
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92. .2320
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/db_xref="taxon:10090"
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Query Best I

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                                                                                                                                                                                                                                                                                                                         Nakamura, K. and Nakamura, T.

Direct. Submission

Submitted (18-FEB-2000) Kenji Nakamura, Osaka Uni
School, Division of Biochemistry, Biomedical Rese
yamadaoka, Suita, Osaka 565-0871, Japan
(E-mail:knakamur@onbich.med.osaka-u.ac.jp,
Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)

Location/Qualifiers
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/translation-"MKDDFAEEEEVQSFGYKRFGIHEGTQCTKCINNMALKFSIVLLY
ILCALLTITVAILGYKVVEKMDNVSDGMETSHQTYDNKLITAVESDLKKLGDQAGKKAL
STNSELSTFSDILDLRGQLQETEKTSKKNVTLEKLQANGDSLVDRGSQLKEFLQNN
SFLITTVNKTLQAYNGYVTNLQQDTNVLQGNLQSQMYSQSVVIMNLNNLNLTQVQQRN
LISNLQQSVDDTSLAIQRIKNDFQNLQQVFLQAKKDYDMLKEKVQSLQTLAANNSALA
KANNDTLEDMNSQLSSTFGQMDNITTISQANEQSLKDLDQDLHKDTENTAVKFSQLEE
RFQVFETDIVNIISNISYTAHHLRTLTSNLNDVMTTCTDTLTRHTDDLTSLNNYLVN
LLDSISLRMQDDMMRSKLDTEVANLSVVMEENKLVDSKHGQLIKKTFILQGPPGPRGP
KGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGTIGFVGPPGPERGSKGSKGSQGPK
GSRGSPGKFGPQGPGSGDMEPLALQNEPTPASEVNGCPPHWKNFTDKCYYFSLE
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/codon_start=1
/product="scavenger receptor
/protein_id="BAB82497.1"
/db_xref="GI:18146952"
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Nakamura, K. and Nakamura, T.
Direct Submission
Submitted (04-DEC-2000) Kenji Nakamura, Osaka University Gradu
School of Medicine, Division of Biochemistry, Biomedical Resea
School of Medicane, Suita, Osaka 565-0871, Japan
(E-mail:knakamur@onbich.med.osaka-u.ac.jp, Tel:81-6-6879-3783,
                                                                                                                                                                                                                                                                                                                                                                             Nakamura,K., Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura,T. Molecular cloning and functional characterization of a human scavenger receptor with C-type lectin (SRCL), a novel member of a scavenger receptor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens SRCL mRNA type II, complete cds. AB052103
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/codon_start=1
/product="scavenger receptor with C-type lectin type II"
/protein_id="BaB39148.1"
/protein_id="BaB39148.1"
/db_xref="qI:1336553"
/translation="MKDDFAEEBEEVPSFGFKREGIHEGTQCPKCHNNWALKFSIILLY
ILCALLTITVAILGYKVVEKMDNVTGGMETSRQTYDDKLTAVESDLKKLGDQTGKKAI
                                                                                           /gene="SRCL"
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/db_xref="taxon:9606"
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SFLITTVNKTLQAYNGYVTULQQDTSVLGGNLQNGYSGNKVYTUNLNNLNLTYGYQGRU
LITHLQRSVDDTSQALGRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTLAANNSALA
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RRGDRGSNGLMRSRLDTEVANLEVNIMEENKLVDSKHGQLIKNFTILQGPPQFRG
RGDRGSOGPPGPTGNKGQKGEKGEPGPPGPAGERGPIGPAGPPGERGKGSKGSQGPK
GSRGSPGKPGPFGFPGFBCKGEFGPGFBGERGPFGFCGLQGTVGEPGVPGPRGLPG
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baldwin, J., Barna, N., Beckerly, R., Boguslavkly, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Lehoczky, J., Lieu, C., Looke, K., Macdonald, P., Marquis, N.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J.,

McEwan, P., McGurk, A., McKernan, K., WcLaughlin, J., Meldrin, J.,

McEwan, P., McGurk, A., McKernan, K., WcLaughlin, J., Meldrin, J.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X.,

Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X.,

The Markey A., Wassillev, H., Vo, A., Wheeler, J., Wu, X.,

The Markey A., Wassillev, H., Vo, A., Wheeler, J., Wu, X.,

The Markey A., Wu, Y., Wassillev, H., Vo, A., Wheeler, J., Wu, X.,

The Markey A., Wu, Y., Wassillev, H., Vo, A., Wheeler, J., Wu, X.,

The Markey A., Wu, Y., Wassillev, H., Vo, A., Wheeler, J., Wu, X.,

The Markey A., Wu, Y., Wassillev, H., Vo, A., Wheeler, J., Wu, X.,

The Markey A., Wu, Y., Wassillev, H., Vo, A., Wheeler, J., Wu, X.,

The Markey A., Wassillev, H., Wassillev,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted (20-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 9, 2000 this sequence version replaced gi:6649269.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Center clone name: 324_G_2
Center clone name: 324_G_2
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     NOTE: This is a 'working draft consists of 8 contigs. The true
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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49221 49320: gap of 100 bp
49321 66394: contig of 17074 bp in length
66395 66494: gap of 100 bp
66495 91692: contig of 25198 bp in length
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                                                                                                                                                                                                                                          490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japa (E-mail:hattoriégsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-DEC-1999) Masahira Hattori,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Only in Database (1999)
2 (Dases 1 to 188439)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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                                                                                                                                                                                                                                                                                                                               Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Canppiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Fersestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Ciliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., WcCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zodv, M.
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                                                                                                                                                                                                                            Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                           Direct Submission
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1 (bases 1 to 71044)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-179K3
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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t, A.F.A. & Green, P. (1996-1997)
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                                                     Center: Whitehead Institute/ MIT Center Center code: WIBR
Contact: sequence_submissions@genome.wi.mit.edu
                             Web site: http://www-seq.wi.mit.edu
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sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
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                                                                                                                                                                                                                                                                                                                                                                                                                          14196 14881: contig of 691 bt
14196 14881: contig of 686 bp
14882 14981: gap of 100 bp
14982 15674: contig of 693 bp i
15675 15774: gap of 100 bp
15775 16460: contig of 686 bp it
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11810 12511: contig of 702 bp

12512 12611: gap of 100 bp

12612 13304: contig of 693 bp

13305 13404: gap of 100 bp

13405 14095: contig of 691 bp
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Center clone name: 179_K_3
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37 3156: gap of 100
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5 22017: contig of 6
8 22117: gap of 11
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40: gap of 100 bp
18836: contig of 696 bp
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44 30745: contig of 702 bp in 14
45 30845: gap of 100 bp
46 31535: contig of 690 bp in 14
36 31635: gap of 100 bp
36 32329: contig of 694 bp in 14
36 32329: contig of 695 bp in 14
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JOURNAL REFERENCE

AUTHORS

TITLE

TITLE JOURNAL

Direct Submission
Direct Submission
Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 178022)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 178,022 genomic DNA of 18p11.3

Published Only in DataBase (1999)

2 (bases 1 to 178022)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                               178022 bp DNA linear HTG 30-MAY-200
Homo sapiens chromosome 18 clone RP11-683J11 map 18p11.3, WORKING
DRAFT SEQUENCE, 20 unordered pieces.
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COMMENT

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Sequence updated (24-Dec-1999)
Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997403.
                                                                                                                                                                                     * runs of N, but the exact sizes of the gaps are unknown that it record will be updated with the finished sequence as soon as it is available and the accession number with the preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: HumDraft18 Center clone name: RP11-683J11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: hattori@gsc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: RIKEN Genomic
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                            10069 110168:
                                                                                                         65059 65158:
                                                                                                                                     46876 46975:
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                           46975: gap of 100 bp
65058: contig of 18083 bp in length
65158: gap of 100 bp
81322: contig of 18164 bp in length
81422: gap of 100 bp
98823: contig of 17401 bp in length
98923: gap of 100 bp
110688: contig of 11145 bp in length
110688: contig of 11145 bp in length
                                                      98923:
                                                                                 81422:
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46875: contig of 22492 bp in
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176271 contig
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169986: contig of 2406 bp in
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34911 c 36303 g 50935
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /chromosome="18"
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                                                                                                                    and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AP001022 187635 bp DNA linear HTG 30-MAY-2
Homo sapiens chromosome 18 clone RP11-815L4 map 18p11.3, WORKING
DRAFT SEQUENCE, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; Hominid 1 (bases 1 to 187635)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hor Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Homo sapiens 187,635 genomic DNA of 18p11.3
                                                                                                    On May 31, 2000 this sequence version replaced gi:6997772
                                                                                                                                                                                                                        Submitted (05-JAN-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                              Published Only in DataBase (2000)

2 (bases 1 to 187635)

Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens DNA, clone: RP11-815L4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP001022.2 GI:8117692
Web site: http://hgp.gsc.riken.go.jp/Contact: hattori@gsc.riken.go.jp
                                         Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTGS_PHASE1;
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                                                                               --- Genome Center
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                                                                                                                                                                                                                                                                                                                                                                                                                            Primates; Catarrhini; Hominidae;
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Pred. No. 1.6e-99;
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                                                                                                                                                                                                                                                                                                                                                                  Hong-Seog, P., and Sakaki, Y.
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Center project name: HumDraft18
Center clone name: RP11-815L4
Center clone name: RP11-815L5
Sequencing vector: PCR products; 100% of reads
Chemistry: Dye-terminator ET-amersham; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 167192 bases at least Q40
Consensus quality: 177020 bases at least Q30
Consensus quality: 187105 bases at least Q20
Insert size: 184435; sum-of-contigs
Quality coverage: 4.35x in Q20 bases; sum-of-contigs
NOTE: This is a 'working draft' sequence. It currently consists
Note: The true order of the pieces is not known and the
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NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved 1 21332 contig of 21332 bp in length

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Sequence updated (26-May-2000).

\* NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 21332: contig of 21332 bp in length 21332 app of 100 bp 100

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misc_feature
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126569 131619: contig of 5051 b
131620 131719: gap of 100 bp
131720 136810: contig of 5091 b
136811 136910: gap of 100 bp
136911 139925: contig of 3015 b
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171271 171370: gap of
171371 174092: cont
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156500 158933: contig of
158934 159033: gap of
159034 161884: contig of
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149003 152918: contig of
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/db_xref="taxon:9606"
/chromosome="18"
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Eukaryota; Eutheria; Primates;
1 (bases 1 to 188255)
                                                                                         AP000939.3 GI:8119080
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-839023
                                                                                                                                                                                               AP000939 188255 bp DNA linear HTG 30-MAY-2000 Homo sapiens chromosome 18 clone RP11-839023 map 18p11.3, WORKING DRAFT SEQUENCE, 32 unordered pieces.
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149003. .152918
/note="assembly_fragment"
153019. .156399
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131720. .136810
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140026. .144232
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136911. .139925
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113290. .120559
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99611. .107273
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120660. .126468
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126569. .131619
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100.0%; Pro
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                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hpp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
On May 31, 2000 this sequence version replaced gi:6997751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 188,255 genomic DNA of 18p11.3

Published Only in DataBase (1999)
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                  182836
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148740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Web site: http://hgp.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: RIKEN
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and Sakaki, Y.
   FEATURES
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158921: contig
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179857: cont
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178531: contig
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119201: contig of 6052
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185810: contig
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51010: contig of 17121
110: gap of 100 bp
63558: contig of 12448
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361 ATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATTATGGAAGAAATGAAG
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                                          AATAATACCCTGGCCAACATCCGTTTGGATTCTGTTTCTCTCAGGATGCAACAAGATTTG
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84838. .90909
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Search completed: March 21, 2003; 06:35:22 Job time: 4123.17 secs

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2: /SIDSZ/gcgdata/geneseq/geneseqn-embl/NA1981.DAT: *
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                                                                                                                                                                                                                                                                                                         New collectin of human origin having antibacterial and antiviral activity, and gene encoding it useful for production of transgen animals and of antibodies for screening potential drug molecules
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               AATAATACCCTGGCCAACATCCGTTTGGATTCTGTTTCTCTCAGGATGCAACAAGATTTG
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Nucleotide

of

a human

scavenger

receptor

Human; scavenger receptor; SRCL-P1; macrophage; basal immunity; arteriosclerosis; diabetes; bacterial infection; restenosis; an low density lipoprotein; ss.

angioplasty;

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                                                                                                                                                                                                                                                                                                          immunity. They are also useful in the treatment, prevention, diag and investigation of diseases such as arteriosclerosis, diabetic complications, bacterial infection and restenosis following angio which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products in
                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a human scavenger receptor, designated SRCL-Pl. The SRCL-Pl polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal
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DB; AAG63346.
AATAATACCCTGGCCAACATCCGTTTGGATTCTGTTTCTCTCAGGATGCAACAAGATTTG
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09-JUL-2000;
19-JUL-2000;
                                                                                                      The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM8642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity. Chemotactic/chemokinetic activity, hemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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19-OCT-2000;
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                                                                                                           EXMAD-6, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12, EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19, EXMAD-20, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are useful in the prevention and treatment of cancers, cell proliferation, cardiovascular, reproductive, immune, musculoskeletal, developmental and gastrointestinal disorders and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bandman
Azimzai
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                                                                                                                                                                                                     The present invention provides the protein and coding sequences for 2 novel extracellular matrix and adhesion associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-7, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12,
                                                                                                                                                                                                                                                                                                                   Isolated polynucleotide encoding extracellular matrix or adhesion-associated protein (EXMAD) useful for diagnosing, treating, preventing disorders associated with expression of EXMAD such as proliferative, immune and genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory; antibacterial; immunosuppressive; antiparkinsonian; neuroprotective; nootropic; osteopathic; haemostatic; vasotropic; antiulcer; fungicide; antidiabettic; antiasthmatic; antiallergic; immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection;
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                                                                                   Novel secreted or transmembrane protein and protein, useful for diagnosis and treatment cancer, autoimmune diseases, bone disorders
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Alzhemer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis. (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders or periodontal disease. (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present of the protein is that of a polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary deoxyribonucleic acid (cDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or ameliorating a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antiinflammatory, stem cell growth factor activity and activin or inhibin-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or genetic disorders. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of
Sequence 2929 BP;
901 A; 699 C; 692 G;
637 T; 0 other;
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Query Match Best Local S Matches 1370; Similarity Conservative 99.9%; Score 1369.4; Pred. No. 0; 0; Mismatches 0; DВ 1; 24; Length Indels 0; Gaps 0;

Ωy Вb Š Db Ş DЬ δÃ 1041 121 981 61 GCCATCAAGTTCAACCAACTGGAGGAACGCTTCCAGCTCTTTGAGACGGATATTGTGAAC ATGAACAGCCAGCTCAACTCATTCACAGGTCAGATGGAGGAACATCACCACTATCTCTCAA GCCAACGAGCAGAACCTGAAAGACCTGCAGGACTTACACAAAGATGCAGAGAATAGAACA GCCATCAAGTTCAACCAACTGGAGGAACGCTTCCAGCTCTTTGAGACGGATATTGTGAAC GCCAACGAGCAGAACCTGAAAGACCTGCAGGACTTACACAAAGATGCAGAATAGAACA . 120 980 1040 1100 60 240 180

1101 181 ATCATTAGCAATATCAGTTACACAGCCCACCACCTGCGGACGCTGACCAGCAATCTAAAT ATCATTAGCAATATCAGTTACACAGCCCACCTGCGGGGCGCTGACCAGCAATCTAAAT

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241 GAAGTCAGGACCACTTGCACAGATACCCTTACCAAACACACAGATGATCTGACCTCCTTG

1161 301 AATAATACCCTGGCCAACATCCGTTTGGATTCTGTTTCTCTCAGGATGCAACAAGATTTG GAAGTCAGGACCACTTGCACAGATACCCTTACCAAACACACAGATGATCTGACCTCCTTG 360

1221 361 1280

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Claim

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                                                                                                                                                                                              This sequence encodes a human secreted protein of the invention. CC This DNA sequence was isolated from a human adult brain cDNA collibrary, and was designated clone bv27_1. The DNAs and proteins cC library, and was designated clone bv27_1. The DNAs and proteins cC are predicted to have biological activities which would make them collibrary although no supporting data is given. Suggested activities include nutritional sources or supplements, immune cc stimulating or suppressing activity, haematopoiesis regulating activity, clissue growth activity, activity, haematopoiesis regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cc receptor/ligand activity, anti-inflammatory activity, cadherin/tumour clivasion suppressor activity, and tumour inhibition activity. The DNAs care also stated to be useful for gene therapy. A host cell transfected with the DNA, or its subfragments and variants is useful for recombinant control.
                                                                                                                                           Query Match
Best Local Similarity
Matches 1370; Conserv
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04-JUN-1997;
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McCoy JM,
1041
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       The invention relates to human nucleic acids (AAI57798-AAI61369) and CC the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful CC in gene therapy. A composition containing a polypeptide or polynucleotide CC of the invention may be used to treat diseases of the peripheral nervous System, such as peripheral nervous injuries, peripheral neuropathy and CC localised neuropathies and central nervous system diseases, such as CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic Clateral sclerosis, and Shy-Drager Syndrome. Other uses include the CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic CC and thrombolytic activity, cancer diagnosis and therapy, drug screening, cassays for receptor activity, arthritis and inflammation, leukaemias and CC c.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed constraints.
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
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ID ABL95574
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24-CCT-2000
08-NOV-2000
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20-DEC-2000
21-DEC-2000
21-DEC-2001
28-FEB-2001
28-FEB-2001
01-MAR-2001
01-MAR-2001
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25-JUL-2000;
25-JUL-2000;
25-JUL-2000;
28-JUL-2000;
02-AUG-2000;
17-AUG-2000;
23-AUG-2000;
24-AUG-2000;
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2000US-22064P.
2000US-22064P.
2000US-220595P.
2000US-0644657.
2000US-033328.
2000US-33978P.
2000US-033928.
2000US-0664610.
2000US-066335.
2000US-0799238.
2000US-0799238.
2000US-0799238.
2000US-0799238.
2000WS-US33673.
2000WS-US33673.
2000WS-US34955.
2000US-076693.
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2001WS-0796498.
2001US-0786520.
2001US-0866566.
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iac hypertrophy; gene therapy; endotheli
antiangiogenic; hypotensive; vulnerary;
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tion; wound; endothelial

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25 - MAY - 2001

30 - MAY - 2001

30 - MAY - 2001

01 - JUN - 2001

28 - JUN - 2001
                                                                                                                                                                                The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
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Godowski I
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(FERR/)
(FERR/)
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                                                                                                                                                                    Sequence
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1369; Conserv
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                                                                                                         ATGAACAGCCAGCTCAACTCATCACAGGTCAGATGGAGAACATCACCACTATCTCTCAA
                                  GCCATCAAGTTCAACCAACTGGAGGAACGCTTCCAGCTCTTTGAGACGGATATTGTGAAC
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         ATCATTAGCAATATCAGTTACACAGCCCACCACCTGCGGACGCTGACCAGCAATCTAAAT
                                                             GCCAACGAGCAGAACCTGAAAGACCTGCAGGACTTACACAAAGATGCAGAATAGAACA
                                                                                               ATGAACAGCCAGCTCAACTCATTCACAGGTCAGATGGAGAACATCACCACTATCTCTCAA
GCCATCAAGTTCAACCAACTGGAGGAACGCTTCCAGCTCTTTGAGACGGATATTGTGAAC
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) STEPHAN J F.
) WATANABE C K.
WILLIAMS P M.
WOOD W I.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
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PAONI
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2001US-0816744.
2001US-0828366.
2001US-0854208.
2001US-0856028.
2001US-0866028.
2001US-0866034.
2001US-0866034.
2001US-0870574.
2001WO-US17092.
2001WO-US17443.
2001WO-US179800.
2001WO-US19692.
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L, Hillan KJ, Marste
CK, Williams PM, Woo
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Pred. No. 0;
0; Mismatches
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Marsters SA,
PM, Wood WI,
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                                                GAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCATA
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   Baker KP,
Godowski
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosin a cardiovascular, endothelial or anglogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, myocardial infarctions, thrombophiebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABL88259 to ABL88267 represent primers and probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 ABB85003. The PRO proteins and polynucleotides have cardiant, cantiangiogenic, hypotensive, vulnerary and antiarregrosclerotic
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CCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAAGGCTCCCAG
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DB; AAG63347.
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                                            Human; chromosome mapping; gene mapping; gene therapy;
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fifth the printed specification.
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23-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                    TCCAGTGGGGACCCAGGCCCCCCGGGCCCACCAGGCAAAGAGGGGACTCCCCGGCCCTCAG
                                                               CCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGCCCTCAG
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                                                                                                                       AAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTTGGGAAGCCCGGCCCTCAGGGC
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New Scavenger receptor proteins SRCL-P1 with collectin-like useful for treatment and diagnosis of diseases associated wi

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Best Local
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                                                                                                       AAGGGACAGAAAGGAGAGAGGGGGAGCCTGGACCACCTGGCCCTGCGGTGAGAGAGGC
                                                                                                                                                   GCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCAACTGGCAAC
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                      GGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCCGGCCCTCAGGGCCCCCAGTGGGGAC
                                                                                                                                       GGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCAACTGGCAAC
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                                                                 CCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAAGGCTCCCAG
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13-AUG-1997;
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  Tokino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence encodes the human cellular stress response 3 (CSR3) protein of the invention. The CSR proteins are macrophage scavenger receptor proteins. The CSR proteins can be used in the treatment, gene therapy and diagnosis of diseases in which intracellular stress is important, such as arteriosclerosis, diabetic circulatory obstruction, and microbial infection. Expression of the proteins is induced in vivo in response to intracellular stress, and inhibits cell death as a result of such stress.
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                 CCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGCCCTCAGGGCCCTCCTGGCTTCCAGGG
                                                                                                                                                                                           GAAAGGAGACCCCGGCATCTTGGGCCCCCTGGGACCCCCAGGGTCCTCAGGGGCAACCTGG
                                                                                                                                                                                                                             GAAAGGAGAGAAGGGGGAGCCTGGACCACCTGGCCCTGCGGGTGAGAGAGGCCCCAATTGG
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                                                                                   AGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGTGGGGACCCAGGCCC
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                                                   AGGCTCAAAGGGCAGCTTTGGAACTGGAGGGCCGAGAGGACAGCCAGGCCCAAAAGGGGGA
                                                                                                                       AGAGGCCGGGCCTGTGGGAGAAAGGGGCCCTGTTGGCCCTCGAGGGTTCCCAGGCCTCAA
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Matches 484
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Search completed: March Job time: 298.589 secs 21, 2003, 02:19:04

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Result
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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Best Local Similarity 53.9
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Like		Sequence 40, Appl Sequence 1, Appli Sequence 66, Appl Sequence 372, App Sequence 624, App Sequence 624, App Sequence 624, App Sequence 633, App Sequence 1, Appli Sequence 94, Appl Sequence 10, Appli Sequence 10, Appl Sequence 63, Appl Sequence 63, Appl Sequence 63, Appl Sequence 96, Appl Sequence 970, Appl

465 ACTACAAGGTCCACCGGGCCCCAGGGGTCCCAAGAGGTGACAGAGGATCCCAGGGACCCCC 524

8.9%; 53.9%;

Score 121.6; DB 1; Pred. No. 4.1e-23; 0; Mismatches 214;

Indels 0; Length

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                                                                                                                   REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A555
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
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                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETTEM 1
                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: CARPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
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                              TOPOLOGY: linear
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 DESCRIPTION:
                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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RESULT 3
US-08-655-086-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
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APPLICANT: GRUSKI
TELEFAX: 51
INFORMATION FOR
                                                                                        APPLICATION NUMBER: US/08
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S.
                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                          TELECOMMUNICATION INFORMATION: 516-228-8484
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                                                             REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 Binding Proteins
NUMBER OF SEQUENCES: 95
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                                APPLICATION NUMBER: US/0
FILING DATE: 02-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                  COMPUTER READABLE FORM:
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CITY: B
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                                                                                                                                                                                                                       COUNTRY: U
ZIP: 02109
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                                                                                                                                                                                                                                                            STATE:
 NAME: Vincent, Matt. REGISTRATION NUMBER:
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52.5%;
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36,709
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US-08-642-255-48
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                                                                                                                                                                    APPLICANT: CAPPELLO, CORPETION APPLICANT: FERRARI, Franco A.

TITLE OF INVENTION: High Molecular Weight Co.

TITLE OF INVENTION: Protein Polymers

NUMBER OF SEQUENCES: 135

CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTO!
ADDRESSEE: FLEHR, HOHBACH, Suite 3400
                                                                                                                                                                                                                                                                                                                        Patent No. 5773249
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Sequence 48, Application US/08642255 Patent No. 5773249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227,7400
                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: DOS
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SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                               STATE:
                                                                                                                           COUNTRY:
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Similarity 53.8%;
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                  Version
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APPLICATION NUMBER:

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                                                                                                                      GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER
TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VEI. 2.0
SOFTWARE: PATENTIN VEI. 2.0
                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/09029348 Patent No. 6171827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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TELEFAX: (415) 494-8771
TELEX: 910 277299 FM UR
INFORMATION FOR SEQ ID NO: 48
OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: DERIVED FROM cDNA OF PROCOLLAGENS
                                         FEATURE:
                                                         ORGANISM: Artificial Sequence
                                                                                   LENGTH: 1608
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
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REFERENCE/DOCKET NUMBER: A5
TELECOMMUNICATION INFORMATION:
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STRANDEDNESS: double
TOPOLOGY: linear
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54.0%;
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Pred. No. 4.5e-19;
0; Mismatches 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 432;
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REFERENCE/DOCKET NUMBER: 36,709
; TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-253-155A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/08253155A Patent No. 5691147 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,7
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gyuris, Jeno
APPLICANT: Draetta, Giulio
TITLE OF INVENTION: CDK4 B!
NUMBER OF SEQUENCES: 95
                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                  STREET: 60 St
CITY: Boston
                                                                                                                                                                    FILING DATE: 02-JUN-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 02109
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Pred. No. 8e-19;
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US-08-494-168-1
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Collagen COL4
TITLE OF INVENTION: of Detecting
NUMBER OF SEQUENCES: 10
                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
FILING DATE: 27-AUG-199: ATTORNEY/AGENT INFORMATION:
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                                                                     CLASSIFICATION: 435
                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W., CITY: Washington, D.C. COUNTRY: USA
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les 226; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCACCAACATCAATGCCACCGACAACCACGCGCACAGCATGCTCATGTACCTGGATGA
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                                                                                                                                                                                                                               20007-5109
                                                                                                                                                                                                                                                                                                                                    Zhou, Jing
NVENTION: Collagen COL4A6: Gene, Protein and Method
NVENTION: of Detecting Collagen Deficiency
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                                                                                                    US/08/494,168
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Pred. No. 7e-
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Best Local Similarity
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                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Reeder
APPLICANT: G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3...
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto:
                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Yale University,
STREET: 246 Church Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        2680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2380 AAATGGTGCTCCGGGGGAACAÁGGCCTACAAGGATTAACAGGGCACAAAGGATTTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
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LOCATION:
                                                                 ZIP:
                                                                                   COUNTRY:
                                                                                                                     CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATCTCAGGACATCCTGGAAAGAAAGGAACAAGAGGCAAGAAAGGTCCTCCTGGATCAAT 2679
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                                                                                                                                                                                                                                                                                                                                                                                                                     TCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCCCGG
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                                                                                                                     New Haven
                                                                                                  Connecticut
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                                                                                 U.S.A.
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                                                                                                                                                                                                                                                    Reeders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              join(2..82, 86..97, 101..4399, ..4465, 4469..4876, 4880..5101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%; 52.4%;
                                                                                                                                                                                                  Alpha-3 Chain Type IV Polynucleotides
 Macintosh OS7.0
                                                                                                                                                                                                                                                 Stephen T., Morrison,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>--</u>
                                3.50 inch, 800K storage
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Pred. No. 5.3e-17;
0; Mismatches 200
                                                                                                                                                   Office of Cooperative Research
                                                                                                                                                                                                                     Collager
                                                                                                                                                                                                                                                      Karen
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CLASSIFICATION: 424
PRIOR APPLICATION DATA: NO. 4
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
2018(
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28180
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
TELEPAX: (212) 370-1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA:
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LIBRARY: Bovin
CLONE: KMC15
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TELEFAX: Y-
TEX: 236268
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hes 228;
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CELL TYPE: Whole kidney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN: Unknown INDIVIDUAL ISOLATE: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                    CCTGGCCCATCAGGAGCGGTGG 913
                                                                                                                                                                                                                                     CCCGGGCCCCCAGGACCACCAGGAGATCCAGGACCCTGTGGGCCAAAAGGTAAACCAGGG
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                                                                                                                 GAGGATGGTCCACCAGGAACTCCTGGACCAACTGGAGAAAAAAGGCAACAAAGGTTGTAAA
                                                                                                                                                                                              CCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGACCTCGG
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                                                                                                                                                                                                                                                                                                                  TCCCTTCCAGGAAGCCCAGGCCCACCTGGTTCAGCTGGAGAACCAGGGATGCAAGGAGAA 522
ACTGGACCACCTGCAGCAGGGG
                                                                           GGAGAGCAAGGACCACCTGGATCCGATGGCCTGCCAGGCTTGAAGGGGGAAACCTGGAGAC
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Similarity 51.6%;
28; Conservative
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KMC15
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lo. 5424408 known
No. 5424408e
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Pred. No. 3.9e-17;
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RESULT 11
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; LOCATION: (1)..(1416)
US-08-399-889-1
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US-08-399-889-1
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                                                                                                Sequence 1, Application US/09167364
Patent No. 6007980
GENERAL INFORMATION:
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Best Local Similarity
Matches 228; Conserv
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APPLICANT: Reeders, Stephen
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APPLICANT: Reeders, Stephen T
APPLICANT: Morrison, Karen E
APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain
FILE REFERENCE: 951263B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/08/39,889B CURRENT FILING DATE: 1995-03-07 EARLIER APPLICATION NUMBER: 07/621091 EARLIER FILING DATE: 1990-11-30 NUMBER OF SEQ ID NOS: 25 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Morrison, Karen E
APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen
FILE REFERENCE: 951263A
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TYPE: DNA
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                                                                                                                                                                                                                                                                      892 CCTGGCCCATCAGGAGCGGTGG 913
                                                                                                                                                                                                                                                                                                                                 643
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                                                                                                                                                                                                                                                 ACTGGACCACCTGCAGCAGGGG
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51.6%;
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Pred. No. 3.9e-17;
0; Mismatches 214;
                    Туре
                       IV Collagen Polypeptides
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Query Match

Length

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; NAME/KEY: CDS
; LOCATION: (1)..(1416)
US-09-167-364-1
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                                                                                                                                                                                                                                                        Sequence 1, Application US/09439897 Patent No. 6277558 GENERAL INFORMATION:
                                                                                 CURRENT APPLICATION NUMBER: US/09/439,897
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENCTH: 1416
TYPE: DNA
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Best Local
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NAME/KEY: CDS
LOCATION: (1)..(1416)
-09-439-897-1
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CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 08/399889
EARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                      APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 95-1263-C
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                                                                  ORGANISM: Bos taurus
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TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application Patent No. 5691197
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                                                                                                                                        COUNTRY: U.S.A.
2IP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3
MEDIUM TYPE: 720 Kb sto
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                               CURRENT APPLICATION DATA
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                                                                                                            COMPUTER: IBM PS/
OPERATING SYSTEM:
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STREET: Suite 700
                                                                                            SOFTWARE:
                                               FILING DATE:
                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                              CITY:
                                                                                                                                                                                                                                                                                        ADDRESSEE: Fay, Sharpe, Bea ADDRESSEE: Minnich & McKee
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Minnich,
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                                                                                              Word Perfect 5.1
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Polypeptide Chain Encoded
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Model 35 s
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                                                                                   Patent No. 6063901

TITLE OF INVENTION: ITTLE OF INVENTION:
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                                                                                                                                                                                                                                                                         Sequence 1, Applic Patent No. 6063901
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Best Local
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: Linear
MOLECULE TYPE: Nucleotide-genomic I
MVPOTHETICAL: No. 5691197 relevant
                                                                                                                                                              TITLE OF INVENTION:
ent No. 6063901
                                                                                                                                                                                                    APPLICANT:
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                                                   CORRESPONDENCE ADDRESS:
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                                                                        NUMBER OF SEQUENCES:
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TYPE: Nucleic acid
STRANDEDNESS: Single
ADDRESSEE: Fay, Sharpe, Beall, Fagan, ADDRESSEE: Minnich & McKee STREET: 1100 Superior Avenue
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                                                                                                                                                                                                                                                                                            Application US/08893467A
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Elomaa, Outi
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a Collagenous Domain and the
Polypeptide Chain Encoded by
such a Sequence
                                                                                                                                                                                 An Insolated DNA Sequence For
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Pred. No. 4.9e-17;
0; Mismatches 216;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TRN
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
MEDIUM TYPE: 720 Kb s
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LENGTH: 1868 base pair
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NAME: Minnich, Richard J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Nucleic acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
ZIP: 44114-2518
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CTTCCTGGGCCAGCAGGACCCCCGG 1165
                 CCTCCTGGCCCATCAGGAGCGGTGG
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                                                                 CCAGGCCCTCAAGGTGCACCAGGACTTTCAGGTGCCAAGGGTGAGCCAGGACGCACTGGT
                                                                                                 GGTTTGGCTGGATCTCCAGGAGTCAAAGGTGACCAAGGAAAACCTGGAGTGCAGGGTGTT
                                                                                                                                                                   GGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGGTGCCTGGACCT 828
                                                                                                                                                                                                       CCCATGGGGTCCCCTGGAGCTCAGGGAGGTAAAGGTGATGCTGGAAAACCAGGCCTACCA 1020
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(216) 241-1666
216) 980162
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No. 6063901 relevant
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RESULT 15 US-08-555-669-11

Sequence 11, Application US/08555669 Patent No. 5773248

GENERAL INFORMATION:

Richard G.

TITLE OF INVENTION: APPLICANT: Brewton, kichard APPLICANT: Mayne, Richard

TYPE IX COLLAGEN AND FRAGMENTS THEREOF

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Matches 229
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 has
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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649 AAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCCGGCCCTCAGGGC
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                                                                                         769 GGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGACCT 828
                                                                                                                            824 GCGCCTGGGAAAGCGGGTGACCGAGGCGAGAGGGGGCCCAGAAGGGTTCCGCGGCCCCAAG
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LOCATION:
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nes 229; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
STATE: New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Halluin, Albert P. REGISTRATION NUMBER: 25,227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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  889 CCTCCTGGCCCATCAGGAGCGGTGG 913
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Search completed: March 21, 2003, 08:25:41 Job time: 61.326 secs

В

1004 GAGGCTGGTCGCAACGGTGCTCCGG 1028

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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9 US-09-926-600A-57
19 US-09-925-307-64
10 US-09-925-307-64
10 US-09-925-307-3947
10 US-09-925-307-3947
10 US-09-925-39-206
10 US-09-925-299-206
11 US-09-951-897-33
11 US-09-954-854A-255
12 US-09-954-854A-255
13 US-09-954-854A-256
14 US-09-954-854A-256
15 US-09-954-854A-256
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17 US-09-954-456-786
18 US-09-954-456-762
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Sequence 198, App
Sequence 3946, App
Sequence 57, App1
Sequence 57, App1
Sequence 64, App1
Sequence 42, App1
Sequence 206, App
Sequence 206, App
Sequence 207, App1
Sequence 208, App
Sequence 208, App
Sequence 2094, App1
Sequence 255, App
Sequence 276, App
Sequence 6, App1
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Sequence 6, App1
Sequence 786, App
Sequence 104, App
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## ALIGNMENTS

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID
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                  TCAGGAGCGGTGGTGCCCCTGGCCCTGCAGAATGAGCCCAACCCCGGCACCGGAGGACAAT
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Pred. No. 0;
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; ORGANISM: Homo US-09-954-456-782
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR PPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR PPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,711
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                              Query Match
                                                                                           SOFTWARE: PatentIn v
SEQ ID NO 782
LENGTH: 6728
TYPE: DNA
                                                                                                                              SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 782,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Process TITLE OF INVENTION: Sets FILE REFERENCE: 689290-76
                                                                                                                                                           PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-99-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
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                Score 111;
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Matches

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Gaps

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APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in
FILE REFERENCE: 44921-0028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3946
LENGTH: 6728
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                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Genbank Accession No. US-09-880-107-3946
                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3946, Application US/09880107 Patent No. US20020142981A1 GENERAL INFORMATION:
                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1021
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                                                                                                                                                   467 TACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTG 526
CGGGTGAGAGAGGCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGCGGCAAAGGAT 646
                                          GTCCCCCAGGTCCCCCTGGAAAGAATGGAGATGATGGGGAAAGCTGGAAAACCTGGTCGTC
                                                                                GCCCAACTGGCAACAAGGGACAGAAAGGAGAGAGAGGGGGAGCCTGGACCACCTGGCCCTG 586
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                                                                                                                            TCCAAGGTCCCCCTGGTGAGCCTGGCGAGCCTGGAGCTTCAGGTCCCATGGGTCCCCGAG 780
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53.0%;
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                                                                                                                                                                                                               Score 111; DB 10;
Pred. No. 2.6e-20;
0; Mismatches 210;
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Вb
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US-09-924-340-57
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                                                                                                                                                                                  Best
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                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS
FILE REFERENCE: 91.US2.REG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/293,574 PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/302,277 PRIOR FILING DATE: 2001-66-29 PRIOR APPLICATION NUMBER: US 60/298,698 PRIOR FILING DATE: 2001-06-15
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                                                                                                                                                                                                                                                             NAME/KEY: polyA_site LOCATION: 1118..1133
                                                                                                                                                                                                                                                                                                   NAME/KEY: polyA_signal LOCATION: 1101..1106
                                                                                                                                                                                                                                                                                                                                         LOCATION: 476..964
NAME/KEY: 3'UTR
LOCATION: 965..1133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: 5'UTR
LOCATION: 1..475
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                  495 AAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCAACTGGCAACAAGGGACAGAAAGG 554
                                                                               109
                                                                                                                     435 GCATGGTCAGCTCATCAAGAATTTTACAATACTACAAGGTCCACCGGGCCCCAGGGGTCC 494
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CAGAGGAGGAGCGAGGACCCCAAGGTAACTCCGGTGAGAAGGGCCGACCAGGGATTTCAAGG
                                                                             GCAAGAGCAGGGCCCCCCAGGATCTGAAGGCCTCCCAGGCCCCCCAGGCCCAGCGGGTCC 168
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                                                                                                                                                           11 Similarity 52.0
267; Conservative
                                                                                                                                                                              8.1%;
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                                                                                                                                                         Score 110.6; DB 9;
Pred. No. 1.2e-20;
0; Mismatches 229;
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US-09-992-600A-57
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                                                                                                                                                                                                                                                                                                                             SEQ ID NO 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES
FILE REFERENCE: 91.US4.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/298,698 PRIOR FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: US 60/293,574 PRIOR FILING DATE: 2001-05-25
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PRIOR
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APPLICANT: Tanaka, Hiroaki
                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 09/924,340
                                 FEATURE: polyA_signal LOCATION: 1101..1106
                                                                                                                                                                                                                                                                                        LENGTH: 11
TYPE: DNA
                                                                                                                                                    NAME/KEY: CDS
LOCATION: 476..964
                                                                                             NAME/KEY: 3'UTR
LOCATION: 965..1133
NAME/KEY: polyA_site
                                                                                                                                      FEATURE:
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                                                                                                                                                                                                            NAME/KEY: 5'UTR
LOCATION: 1..475
                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                       FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 60/302,277 FILING DATE: 2001-06-29
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-925-302-64
; Sequence 64, Application US/09925302
; Patent No. US20020044941A1
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US-09-992-600A-57
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Best Local Similarity
Matches 267; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA104
                                                                                                     FEATURE: NAME/KEY: misc feature LOCATION: (2653)
                                     NAME/KEY: misc feature
LOCATION: (2667)
OTHER INFORMATION: n equals a,t,9,
                                                                                                                                                                                               TYPE: DNA
NAME/KEY: misc feature LOCATION: (2683)
                                                                                                 OTHER INFORMATION: n equals
                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                LENGTH:
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52.9%;
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Pred. No. 1.2e-20;
""ematches 229;
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US-09-925-302-64

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US-09-925-301-42
; Sequence 42, Application US/09925301
; Patent No. US20020052308A1
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; ORGANISM: Homo sapiens
US-09-925-301-42
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                                                                                                                                 Query Match
Best Local Similarity
Matches 274; Conserv
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
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Best Local Similarity
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SEQ ID NO 42
LENGTH: 2192
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CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: ECT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PA106
                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                         472 GGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCA 531
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698
                  532 ACTGGCAACAAGGGACAGAAAGGAGAGGGGAGCCTGGACCACCTGGCCCTGCGGGT
                                                                 638 GGCCCCGCTGGACCCCCTGGTGCTCCTGGTGCTCCTGGTGCCCCTGGCCCCCGTTGGCCCT 697
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                                                                                                                                         Conservative
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                                                                                                                                   Score 107.2; DB 10;
Pred. No. 1.6e-19;
0; Mismatches 228;
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CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR EILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATEENTIN VET: 2.1
SEQ ID NO 3947
LENGTH: 5086
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APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Horne, Darci T. APPLICANT: Vockley, Joseph APPLICANT: Scherf, Uwe
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LOCATION: (1)..(5086)
OTHER INFORMATION: n =
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Pred. No. 2.9e-19;
0; Mismatches 235;
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LOCATION: (17)
OTHER INFORMATION: n equals a.
NAME/KEY: misc_feature
LOCATION: (5126)
OTHER INFORMATION: n equals a.
NAME/KEY: misc_feature
LOCATION: (5143)
                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 206
LENGTH: 514
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PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
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LOCATION: (4)
COTHER INFORMATION: n equals a,t,g,
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Pred. No. 2.9e-19;
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SEQ ID NO 206
LENGTH: 5145
                                                                        Query Match
Best Local Similarity
Matches 248; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1556
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TITLE OF INVENTION: Nucleic Acids, Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: PA102
                                                                                                                                                                                 LOCATION: (5126)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (5143)
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LOCATION: (4)
OTHER INFORMATION: n equals
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LOCATION: (17)
OTHER INFORMATION: n equals
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                                                                      Score 107; DB 10;
Pred. No. 2.9e-19;
0; Mismatches 235;
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTMARE: PERL Program
SEQ ID NO 22
LENGTH: 5432
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.13
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Best Local Similarity
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51.3%;
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; LENGTH: 4908
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-001-887-33
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/244,998
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 7.8%; Score 106.8; DB 9; Best Local Similarity 52.9%; Pred. No. 3.2e-19; Matches 256; Conservative 0; Mismatches 222;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Macina, Roberto
APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: DEX-0269
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                                                                        AGGAGCCCTGGGGCAGAAAGGTGACTTGGGGCTGCCTGGGCAGCCTGGCCTGAGGGGTCC
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US-09-954-531-961
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CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
INUMBER OF SEQ ID NOS: 1392
SOFTWARE: Patentin version 3.0
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LENGTH: 254
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FILE REFERENCE: 689290-77
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ORGANISM: Homo sapiens
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Local Similarity 52.1%;
AGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGAC
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Pred. No. 3.7e-19;
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 255
LENGTH: 2542
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APPLICANT: Horrigan, Stephen
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Best Local Similarity
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Pred. No. 3.7e-19;
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PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
SEQ ID NO 786
LENGTH: 5416
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-786
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PRIOR FILING DATE: 2000-09-18
PRIOR PPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
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Best Local Similarity 51.1%;
Matches 247; Conservative
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CURRENT FILING DATE: 2001-09-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 689290-76
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Search completed: March 21, 2003, 08:22:21 Job time: 227.91 secs

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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hump
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                   Direct Submission
Submitted (05-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                      Sequencing Center
Center code: BCM-HGSC
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BEF929798 RC3-GN004
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BEF9110880 MR2-EN009
BEF911080 AGENCOURT
BG482931 602502939
AI742661 WG44f06.x
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BB749743 BB749743
BF854188 MR2-EN009
BF854188 MR2-EN009
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B1445844 dai33410.
B1697412 603348154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: amg@bcm.tmc.edu
Gunaratne, P.H., García, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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//tissue_type="Mammary tumor. W Old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DHIOB"
/note="Wector: pcWV-SPORT6"
a 757 c 760 g 757 t
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/db_xref="taxon:10090"
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5', mRNA sequence.
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                                                         Unpublished (1999)
Contact: Robert Strausberg, F
Email: cgapbs-r@mail.nih.gov
                                                                                            1 (bases 1 to 957)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                         house mouse.
Mus musculus
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                CCCCCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGCCCTCAGGGCCCTCCTGGCTTCCA
                                                                   CAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGTGGGGACCCAGG
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quality sequence stop:
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/note="Organ: Olfactory epithelium; Vector:
/note="Organ: Olfactory epithelium; Vector:
pcMv-SpORT6.1.codb; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: ti
is a NIH_MGC Library."
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/clone_lib="NIH_MGC_129"
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/db_xref="taxon:10090"
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Pred. No. 1.7e-156;
0; Mismatches 113;
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                        ATCATTAGCAATATCAGTTACACAGCCCACCAGCGGGACGCTGACCAGCAATCTAAAT
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5', mRNA
BQ891432
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Tissue Procurement: Mark Maconochie,
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
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                                                                                                                                                                                                                                                                                                                                                                                      /clone="IMAGE:6332754"
/clone=lib="NIH_MGC_130"
/clone="DH10B (phage-resistant)"
/note="Organ: otcoysts; Vector: pCMV-SPORT6.1.ccdb;
Site_1: EcoRV; Site_2: Not1; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is
NIH_MGC Library."
a 250 c 244 g 163 t 6 others
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/db_xref="taxon:10090"
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Pred. No. 1.2e-132;
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                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hum
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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NIH-MGC http://mgc.nci.nih.gov/.
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603172765F1 NCI_CGAP_Mam5
mRNA sequence.
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http://lmage.llnl.gov
Plate: LLAM11636 row: b column: 17
                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                   National Institutes of Health,
Unpublished (1999)
                                                                                                                                                                                                                                           Mus musculus
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                                                                                                                                                                                                                                                     house mouse
                                                                    quality sequence stop: 
Location/Qualifiers
        /organism="Mus musculus"
/strain="C578L/6J"
/db_xref="taxon:10090"
/clone="IMAGE:5251888"
/clone_lib="NCI_CGAP_Mam5"
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1 to 906)
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Rodentia;
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/dev_stage="7 months"
/lab_host="DH10B"
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High quality sequence stop: 598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
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National Institutes of Health, Mammalian Gene
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CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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/tissue_type="epidermoid carcinoma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin
                                                                                                                        /clone="IMAGE:6212672"
/clone_lib="NIH_MGC_102"
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Mammalia; Eutheria;
1 (bases 1 to 967)
                                                                                                                    Li,W.B., Gruber,C., Jessee,J. Full-length cDNA libraries and Unpublished (2001)
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                                                                                                         Contact: Genoscope
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148 c 167 g 137 t
            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODE005YH04"
/clone_lib="LTI_FL002_PL1"
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Eukaryota; Metazoa; Rodentia;
                                 Unpublished (1999)
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National Institutes of Health,
                                                              Mammalia; Eutheria;
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Craniata; Vertebrata; Sciurognathi; Muridae;

Euteleostomi;
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/note="Grgan: placenta; Vector: pcMVSPORT 6; 1st strand /note="Corgan: placenta; Vector: primer. Five prime cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville , Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
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GI:10407765
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                                          GGAAGTGGCTGGATGGGACATCTCCAGACTACAAAAATTG 1214
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Plate: LLAM9128 row: m column: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found through the I.M.A.G.E. Consortium/LLNL at:
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Clone distribution: MGC clone distribution information
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/clone=lib="NCI_CGAP_Maml"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
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Tel: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: johng@tigr.org
Plate: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouackenbush, J. Assessment of gene expression patterns metastasis using a 19,200 element cDNA Unpublished (2000)
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The Institute for Genomic
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Mammalia; 1
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, |
/clone="Vector: pBluescriptSKm"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphre
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Mam5"
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                                                                                                                                                                                        AGCCAACGAGCAGAACCTGAAAGACCTGCAGGACTTACACAAAGATGCAGAGAATAGAAC 119
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   AGCTGTCAAGTTCAGCCAACTTGAGGAACGCTTCCAGGTCTTTGAGACAGATATTGTGAA
                                 AGCCATCAAGTTCAACCAACTGGAGGAACGCTTTCCAGCTCTTTGAGACGGATATTTTGGAA 179
                                                                                                                                   GGCCAACGAGCAGAGCCTGAAAGACCTTCAGGACTTACACAAGGATACAGAAAATAGAAC
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B0934501
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Hioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Dlate: LLAM13785 row: m column: 03
High quality sequence stop: 352.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect Unpublished (1999)
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/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb;
/note="Organ: otocysts; Vector: pCMV-SPORT6.1.ccdb; Vector: pCMV-SPORT6.1.ccdb;
/note="Organ: otocysts; Vector: otocysts; Vector: pCMV-SPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6330794"
/clone_lib="NIH_MGC_130"
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                                                              Bmail: genome-res@gsc.riken.go.jp,
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                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
On Jul 6, 2000 this sequence version replaced gi:8940810.
Contact: Yoshihide Hayashizaki
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EST.
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Iowa
451 Eckstein Medical Research Building Iowa
Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97044477
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              /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR ; Site_2: Not I; UT-F-EJO is a subtracted CDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor; digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CCATTAGCGA; eye anterior segment, AATCCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and
                                                                                                                                                                                                                                                                                                                                                  /clone="UI-E-EJO-ahq-c-05-0-UI"
/Clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Soares,
                                                                                                                                                                                                                                                                                          /dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                                                                                                                                                                                                                                                                                                                                  Choroid"
                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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AUTHORS
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ORGANISM
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                    Location/Qualifiers
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1019 AAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCA 1078
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                                                                                                        Tissue Procurement: Dr. Gregg Hageman CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                       Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
sequence: 443-498, >POLY_A#Simple_repeat
Seq primer: M13 Reverse.
                                                     Genetics (www.resgen.com).
The following repetitive elements were found
                                                                                                                                                                                                                                                                        451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                                                                                                                                                                                                                            msoares@blue.weeg.uiowa.edu
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TAG_SEQ=AATGCCGCAT"
123 c 89 g 179 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 (9), 791-806 (1996)
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    AUTHORS
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                                                                                                                             808 bp mRN?
UI-M-FIO-byu-g-09-0-UI.r1 NIH_BMAP_FIO
IMAGE:5702432 5', mRNA sequence
BQ771366.1 GI:21979842
EST.
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 808)
                                                                                      Mus musculus
                                                                                                             house mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGGGA; eye anterior segment, AATGCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
/clone="UI-EJO-ahq-c-05-0-UI"
/clone_lib="UI-E-EJO"
/clone_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE a
Choroid"
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modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed
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Pred. No. 1.2e-75;
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                                       Euteleostomi; 
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       TTATGCTGGGCAGTGGAACGATTTCCAATGTGAAGACGTCAATAACTTCATTTGCGAAAA 1340
                                                                                                                                                                      GCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTCCAGACTACAAAAATTGGAAAGC 1220
                                                                                                                                                                                                                                                                                                                                                       TGGACAGCCGGATAACTGGGGTCATGGCCCATGGGCCAGGAGAAGACTGTGCTGGGTTGAT 1280
                                                                                                                                                                                                                                        ATGGATAAAAAAACAGATGGTAGGGAGAGAGAGCCACTGGATCGGCCTCACAGACTCAGA 1160
                                                                                                                                                                                                                                                                                                                                                                                                                             GAACTTCACAGATAAATGCTACTATTTTTCATTGGAAAAAGAAATTTTTTGAAGATGCTAA
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                                                     TGGACAACCAGATAACTGGGGCAGTGGCCATGGGCCAGGAGAAGACTGTGCTGGCTTGAT
                                                                                                                                                 ACAGGAAAGCGAATGGAAGTGGCTAGACGGGTCACCTGTTGATTACAAAAACTGGAAAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: pYX-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="DH10B (T1 phage resistant)"
/note="Organ: Brain: Vector: pYX- Asc; Site_1: EcoR I;
/note="Organ: Brain: Vector: pYX- Asc; Site_1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
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/db_xref="taxon:10090"
/clone="IMAGE:5702432"
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/dev_stage="embryo 12.5dpc"
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85.1%;
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Search completed: March 21, 2003, 08:08:10 Job time : 1811.64 secs

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Database

Pred. No. is the number of results predicted by chance to have

em\_htgo\_hum:\*
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em\_htgo\_other:\*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result ν<sub>o</sub>. 4444444333333300544331177654433 1024 1024.4 1024.4 146.8 146.8 129 129 125.8 125.8 124.2 124.2 124.2 124.2 124.2 124.2 124.3 121.6 121.6 121.4 121. 388 388.4 378.4 157.6 157.6 157.6 802 800.4 615.4 488.8 Score Query Match 112.6 112.3 112.3 112.3 112.3 112.3 113.4 113.6 5 189088 5 189088 6 171044 1 187635 5 188255 5 188255 3 193208 3 193208 3 193208 3 193208 1 193208 1 198022 1 188255 5 188255 5 188255 6 19368 756 6114 130763 Length 2983 1886 2005 2005 2641 3058 4628 5676 5676 7138 4581 2010 5551 6109 В 10 10 AF272662 AX239611 ) AF176645 AR014110 CRUPALV AC112416 AB052836 ) MMU16789 AR014116 PALCOL1A AF272661 AF138883 AB008374 AP000900 AP001022 AB078434 AB052103 AB052103 AB052133 AC016128 AP000915 AC024368 AP001022 AP000900 AP000900 AP000900 AP012618 AC112618 AC0112416 AB007829 E32511 AX454442 AX490920 AX047353 AB038518 ECU62528 HUMA2XICOL AB009993 AP000939 AB008683 E07265 IJ HUMPA1V HSM80298 AB005145 AX454442 Sequence AX490920 Sequence AX490920 Sequence AX047753 Sequence AX047753 Sequence AB038518 Homo sap1 AB078434 Mus muscu AB038519 Mus muscu AB038519 Homo sap1 AC016128 Homo sap1 AC016128 Homo sap1 AC012436 Homo sap1 AP000919 Homo sap1 AP000919 Homo sap1 AP000919 Homo sap1 AC012416 Rattus no AB007829 Homo sap1 E32511 Scavenger r E32509 Scavenger r E32509 Scavenger r E32509 Scavenger r E0026446 Mus muscu AP000990 Homo sap1 E32512 Homo sap1 E32513 Scavenger r E0026446 Mus muscu AP000993 Homo sap1 AP001022 Homo sap1 AP001022 Homo sap1 AP001022 Homo sap1 AP001025 Homo sap1 A AB005145 Homo sapi AL713657 Homo sapi AC112416 Rattus Description

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## ALIGNMENTS

AUTHORS	REFERENCE	SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	LOCUS	RESULT 1 AB005145
Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Keshi,H., Sakai,Y., Fukuoh,A., Sakamoto,T., Itabe,H., Suzutani,T., Ogasawara,M., Yoshida,I. and Wakamiya,N.	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens female tissue_lib:placenta cDNA to mRNA.  Homo sapiens  Filtringts Notation Character Companies Voltables Control	AB005145.1 GI:17026100	Homo sapiens CL-Pl mRNA for collectin placenta 1, complete cds. AB005145	AB005145 2983 bp mRNA linear PRI 21-NOV-200	

21-NOV-2001 cds.

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         GCCCCCAGTGGGGACCCAGGCCCCCGGGCCCAGCCAGAAAGAGGGACTCCCCGGCCCT
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                                                 GGCCCCAGTGGGGACCCAGGCCCCCCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGCCCT
                                                                                                                  TCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCCGTGGTTCCCCTGGGAAGCCCCGGCCCTCAG
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                                                                                            TCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAG
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Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College, Submitted (15-JUN-1997) Katsuki Ohtani, Asahikawa Medical College, Department of Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa, Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp, Tel:+81-166-68-2393, Fax:+81-166-68-2399)
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J. Biol. Chem. 276 (47), 44222-44228 (2001)
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                                                                                                  Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the Ger
Genome Broject
                                                                                                                                                                                                                                                                                                                                   AL713657
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at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
                             Please contact the RZPD: Ressourcenzentrum, Heuberlin-Charlottenburg, GERMANY; Email: clone@r: information about the clone and the sequencing
                                                           This clone (DKFZp547G1215) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1409
                                                                                         Genome Project
                                                                                                                                                                                       Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a,
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Koehrer, K., Beyer, A., Mewes, H.W.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae
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GERMANY; Email: clone@rzpd.de Further
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/clone_lib="547 (synonym: hfbr1). Vector pSport1;
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/dev_sytage="fetal"
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/protein_id="CAD28466.
/db_xref="GI:19584340"
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/gene="DKFZp547G1215"
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/organism="Homo sapiens"
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/note="similarity to
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/map="18p11.3"
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Sequence 27
AX454442
AX454442.1
                                                                                            disorders involving angiogenesis
Patent: WO 0208284-A 27 31-7AN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US);
Paoni, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
                                                                                                                                                                                                                                           Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A., Goddwski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
                                                                                   Watanabe, I. (US)
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       /organism="Homo sapiens"
/db_xref="taxon:9606"
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Query Match Best Local Similarity

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Score 1024.4; DB 6; Pred. No. 8.7e-226;

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 GGCCCTCCTGGCCCATCAGGAGCGGTGGTGCCCCTGGCCCTGCAGAATGAGCCAACCCCG
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Sequence
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AX490920.
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Mammalia; E
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/db_xref="taxon:9606"
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J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J
Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood,
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GCATTA
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                                                  ATGGAAGAATGAAGCTAGTAGACTCCAAGCATGGTCAGCATCAAGAATTTTACAATA 120
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AX047353
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 2641)
Bandman,O., Hillman,J.L., Tang,Y.T., Lal,P., Yue,H., Baughn,M.R.,
Lu,D.A. and Azimzai,Y.
                                                                                                                                                                                                                                                  Extracellular matrix and adhesion-associated Patent: WO 0068380-A 39 16-NOV-2000;
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ilarity 99.9%;
Conservative
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Location/Qualifiers
                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 4586187CB1"
a 628 c 608 g 582 t
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Pred. No. 8.8e-226;
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RESULT 6 AB038518 LOCUS

AB038518

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linear

PRI 08-MAR-2001 -type lectin

receptor with

VERSION
KEYWORDS
SOURCE
ORGANISM

Homo

sapiens tissue\_lib:Placenta cDNA to sapiens

mRNA

Metazoa; Chordata; Craniata; Vertebrata;

Euteleostomi;

Eukaryota;

DEFINITION ACCESSION

AB038518.1

Homo sapiens SRCL mRNA for scavenger type I, complete cds.
AB038518

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                                                                                         GATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCAT
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   TCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCCTGGGAAGCCCCGGCCCTCAG
                                                                                                                   GGCCCAACTGGCAACAAGGGACAGAAAGGAGAGAGGGGGAGCCTGGACCACCTGGCCCT
                                                                                                                                                                                               CTACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCT
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                                       GCGGGTGAGAGGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medic School, Division of Biochemistry, Blomedical Research Center; yamadaoka, Suita, Osaka 565-0871, Japan
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Location/Qualifiers
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KEIFEDAKLFCEDKSSHLVFINTEREDQWIKKQNGRESHWICTDSERENEWKWLDG
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                                                      Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Sakai,Y., Fukuoh,A., Sakamoto,T., Itabe,H., Suzu Ogasawara,M., Yoshida,I. and Wakamiya,N. CDNA cloning of mouse CL-P1 gene
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           Fukuoh, A.,
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Submitted (18-FEB-2000) Kenji Nakamura, School, Division of Biochemistry, Biomeo yamadaoka, Suita, Osaka 565-0871, Japan (E-mail: knakamur@onbich.med.osaka-u.ac.; Tel:81-6-6879-3783(ex.3783), Fax:81-6-68
                                                                                                                                                                             Nakamura.K., Funakoshi,H., Tokunaga.F. and Nakamura.T.
Molecular cloning of a mouse scavenger receptor with C
(SRCL)(1), a novel member of the scavenger receptor fa
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
  osaкa-u.ac.jp,
Fax:81-6-6879-3789)
                                                           amura, Osaka Univers
Biomedical Research
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type II, comp
AB052103
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (04-DEC-2000) Kenji Nakamura, Osaka University Gradu School of Medicine, Division of Biochemistry, Biomedical Resea Center; 2-2 yamadaoka, suita, Osaka 565-0871, Japan (E-mail:knakamur@onbich.med.osaka-u.ac.jp, Tel:81-6-6879-3783)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nakamura, K. and Na
Direct Submission
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Mammalia; Eutheria; Primates;
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/gene="SRCL"
//codon_start=1
//codon_start=1
//product="scavenger receptor with C-type lectin type II"
//protein_id="shaB39148.1"
//protein_id="BhaB39148.1"
//db_xref="gI:1336553"
//translation="MKDDFAEEEEVPSFGFKRFGIHEGTOCPKCHNNWALKFSIILLY
//translation="MKDDFAEEEEVPSFGFKRFGIHEGTOCPKCHNNWALKFSIILLY
//translation="MKDDFAEEEEVPSFGFKRFGIHEGTOCPKCHNNWALKFSIILLY
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//translation="MKDDFAEEEEVPSFGFKRFGIHEGTALVOCPKKLGDOCKKLGDOCKKLGDOCKKLGDOCKKLGTOKKLGDOCKKLGTANNALA
STNSELSTFRSDILDLRQCHECTSTSQALGONKOLDGDHKDAGENRTALKFTQLGE
RFQLFETDLWAGILGSTGOMENITTISQANEGNIKOLOGDHKDAGENRTALKFNQLEE
RFQLFETDIVNIISNISYTAHHLRTLTSNLNEVRTTCTDTLTKHTDDLTSLNUTLANI
RLDSVSLRMQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGPPGPRGP
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                                                                                                                                                                                                                                                                       /gene="SRCL"
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/db_xref="taxon:9606"
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Homo sapiens chromosome 18 clone
SEQUENCE, 8 unordered pieces.
 Birren, B.,
                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                               Unpublished
                                              Homo sapiens chromosome
                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                               Homo sapiens
                                                                                                                                                 HOMO
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                  (bases 1 to 169088)
                                                                             (bases 1 to 169088)
                                                                                                                                            sapiens.
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1065 c 1035 g 1044 t
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GSRGSPGKPGPQGPSGDPGPPGPPGKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPG
   Linton, L.,
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 Nusbaum, C.,
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Lander, E.,
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Allen, N.,
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 Anderson, M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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Brown,A., Castle,A., Colangelo,M., Collins,S., Col
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Baldwin,J.,
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Center clone name: 324_G_2
Center clone name: 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeats were identified using RepeatMasker:
t, A.F.A. & Green, P. (1996-1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WIBR Web site: http://www-seq.wi.mit.edu
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Location/Qualifiers
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120869: contig of 29077 bp in
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43: gap of 100 bp

22424: contig of 4381 bp in length

234: gap of 100 bp
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                               sequences.
AP000915
AP000915.5
HTG.
           Homo
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Homo sapiens
 Eukaryota;
                      Homo sapiens DNA, clone:RP11-720L2
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22525. .38094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
17-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
On Apr 26, 2002 this sequence version replaced gi:9188470.

Location/Qualifiers
Homo sapiens chromosome 11 clone SEQUENCE SAMPLING. AC024368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens genomic DNA Published Only in Database (1999) 2 (bases 1 to 188439)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-DEC-1999) Masahira Hattori,
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/db_xref="taxon:9606"
/chromosome="18"
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Watanabe, H. and Sakaki, Y.
                             RP11-179K3 map 11,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M.,
Ferrestra, P., FitzHugh, W., Forrest, C., Gage, D.,
Galagan, J., Gardyna, S., Ginder, S., Goyette, M., Graham, L.,
Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R.,
Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M.,
McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J.,
Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Naylor, J.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M.,
Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C.,
Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S.,
Severy, P., Spencer, B., Stange-Thomann, N., Stojaovic, N.,
Store, S., Traylilo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B.,
Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (28-FEB-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birren, B., Linton, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 71044)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                 NOTE: This record contains 90 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
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                                                                                                                                                                                                                                                        will be sequenced to completion. In the event the record is updated, the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: L6145
Center clone name: 179_K_3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
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85 2384; gap of 100 bp
85 3056; contig of 672 bp
87 3156; gap of 100 bp
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6183:
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3951: gap of 100 bp
4627: contig of 676 bp in
                                                                                                                                                        798: gap of 100 bp
1495: contig of 697 bp in length
1595: gap of 100 bp
2284: contig of 689 bp in length
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5409: cor
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J., Barna,N., Beda,F., ]
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g of 682 bp :
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13998: contig of 684 bp 1
13998: gap of 100 bp
34694: contig of 696 bp 1
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11709: contig of 687 bp
1809: gap of 100 bp
12511: contig of 702 bp
2611: gap of 100 bp
13304: contig of 693 bp
14095: contig of 691 bp
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28355: contig of 6
3455: gap of 10
29145: contig of 6
2245: gap of 10
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2117: gap of
22815: contig c
23609: contig c
23609: contig c
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31535: contig (
635: gap of
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53746: gap of 100 bp
54409: contig of 663 bp in
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38663: contig of 691 bp
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order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence

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as soon as it is available and the

21332 contig

of.

21332 bp in length

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,
Japan (E-mail:hattori@jsc.riken.go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Only in DataBase (2000)

2 (bases 1 to 187635)

3 Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
NOTE: This is a 'working draft' sequence. It currently consists 33 contigs. The true order of the pieces is not known and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URL:http://hgp.gsc.riken.go.jp/,
Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H., Homo sapiens 187,635 genomic DNA of 18p11.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APO01022 187635 bp DNA linear HTG 30-MAY-2000 Homo sapiens chromosome 18 clone RP11-815L4 map 18p11.3, WORKING DRAFT SEQUENCE, 33 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On May 31, 2000 this sequence version replaced gi:6997772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-JAN-2000) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                               Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
----- Project Information
Center project name: HumDraft18
Center clone name: RP11-815L4
                                                                                              Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 167192 bases at least Q40 Consensus quality: 177020 bases at least Q30 Consensus quality: 182105 bases at least Q20 Insert size: 184435; sum-of-contigs
                                                                            Quality coverage: 4.35x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                         Center: RIKEN Genomic Sciences Center(GSC) Center code: RIKEN
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sapiens DNA, clone:RP11-815L4.
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21433 42072 contig of 20640 bp in length
42173 54336 contig of 12164 bp in length
54437 66766 contig of 12330 bp in length
66867 77849 contig of 10983 bp in length
77950 8798 contig of 10983 bp in length
77950 8798 contig of 763 bp in length
107374 113189 contig of 5816 bp in length
112060 120468 contig of 5809 bp in length
120559 contig of 5809 bp in length
131690 contig of 5809 bp in length
131720 131619 contig of 5901 bp in length
131691 contig of 5901 bp in length
144026 144232 contig of 4207 bp in length
144033 148902 contig of 3015 bp in length
14903 152918 contig of 4207 bp in length
150500 15093 contig of 3916 bp in length
150500 15093 contig of 2851 bp in length
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160402 160300 contig of 2851 bp in length
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7950 87798: contig of 9845 ...
7799 87898: gap of
87899 99510: contig of 11612 bp in length
99511 99610: gap of
100 bp
107274 107373: gap of
1013190 113289: gap of
113290 120559: contig of 7863 bp in length
113290 120559: contig of 5816 bp in length
120660 126468: contig of 5800 bp in length
126469 126568: gap of
131620 131719: gap of
131620 131719: gap of
131620 131719: gap of
131621 131719: gap of
131621 131719: gap of
131621 131719: gap of
131720 138811 136910: contig of 5091 bp in length
13928 140025: gap of
14233 144332: contig of 3015 bp in length
144333 144332: contig of 4207 bp in le
144333 148902: gap of
149002: gap of
100 bp
144333: gap of
149002: gap of
100 bp
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2133 2433: gap of 100 bp
21433 42072: contig of 20640 bp in length
42073 42172: gap of 100 bp
54337 54336: contig of 12164 bp in length
54337 54436: gap of 100 bp
54437 66766: contig of 12330 bp in length
66767 66866: gap of 100 bp
66867 77849: contig of 10933 bp in length
77850 87798: contig of 1093 bp in length
77850 87798: contig of 19849 bp in length
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Jap of 1695

Jap of 1695

Jap of 100 bp

179788: contig of 1796 bp

179887 179886: gap of 100 bp

181479: contig of 1592

181479 181578: gap of 100

182896 182995: contig of 1592

182896 182995: gap of 100

182896 184841: cc

184942 184941: cc

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153019 156399: contig of
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136911. 139925
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140026. 144232
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107374. .113189
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87899. .99510
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42173. .54336
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77950. .87798
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54437. .66766
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/chromosome="18"
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126569. .131619
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120660. .126468
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131720. .136810
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113290. .120559
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                                                            and Chemical Research (RIKEN), Genomic Sciences Cent
Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagav
Japan (E-mail:hattori@gsc.riken.go.jp,
URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,
Fax:81-42-778-9924)
                                                                                                                                                                             Direct Submission
Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical Submitted (17-DEC-1999) Masahira Hattori, The Institute 
                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 178022)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 178,022 genomic DNA of 18pll.3
Published Only in DataBase (1999)
2 (bases 1 to 178022)
Hattori,M.; Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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                            May 31, 2000 this sequence version replaced gi:6997403.
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sapiens DNA, clone:RP11-683J11.
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Sequence updated (24-Dec-1999)
Sequence updated (26-May-2000)
* NOTE: This is a 'working draft' sequence. It currently
* Consists of 20 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                                                                                            24283: contig of 24283 bp in le
24284 24383: gap of 100 bp
24384 46875: contig of 22492 hr
46876 46975: gap of
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                                                                                       46876 46975; gap of 100 bp 46976 65058; contig of 18083 bp in le 65059 651.58; gap of 100 bp 65159 81322; contig of 16164 bp in le 81323 81422; gap of 100 bp 81423; contig of 17401 bp in le 98824 98923; gap of 17401 bp in le 98824 98923; gap of 100 bp 98824 110068; contig of 11145 bp in le
110069 110168: gap of 100 bp

110169 122716: contig of 12548 bp in

122717 122816: gap of 100 bp

122817 133089: contig of 10273 bp in

133090 133189: gap of 100 bp

133190 141206: contig of 8017 bp in 1

141207 141306: gap of 100 bp
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Center project name: HumDraft18
Center clone name: RP11-683J11
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46976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://hgp.gsc.riken.
Contact: hattori@gsc.riken.go.j
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Center code: RIKEN
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149151 156105: cont
   Conservative
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46976. .65058
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167581. .169986
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Location/Qualifiers
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174764. .176271
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172010. .172317
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162149. .165118
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CE 1 (bases 1 to 188255)

RS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 188,255 genomic DNA of 18p11.3

AL Published Only in DataBase (1999)

CE 2 (bases 1 to 188255)

RS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

AL Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555,

URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923,

Fax:81-42-778-9924)
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Homo sapiens chromosome 18 clone RP11-839023 map 18p11.3, WORKING
DRAFT SEQUENCE, 32 unordered pieces.
                                                                                                                                                    On May 31, 2000 this sequence version replaced
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Homo sapiens DNA, clone:RP11-839023.
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                                                Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                      Center code: RIKEN
Center project name:
                                                                                                                            Center: RIKEN Genomic
                             ----- Project
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Sequence updated (06-Jan-2000)
Sequence updated (26-May-2000)
* NOTE: This is a 'working draft' sequence. It currently
* NOTE: This is a 'working draft' sequence. It currently
* consists of 32 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                  1 16096: contig of 16096 bp in 16097 16196: gap of 1793 bp in 16197 33789: contig of 1793 bp in 33790 33889: gap of 17912 bp in 18178 2488 bp in 18178 2488 bp in 18178 2488 bp in 18178 2488 bp in 18178 24875 248 bp in 18178 248 bp in 
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1 US-09-439-899-1

1 US-09-439-897-1

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REFERENCE/DOCKET NUMBER: A555
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEPAX: (415) 494-8771
TELEPAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 50, Application US/08642255 Patent No. 5773249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
                                                                                                                                                                                                                                           FILING DATE:
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, BETCTAM I
                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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CITY: 9
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   DESCRIPTION:
                                    TOPOLOGY:
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                                                                                        LENGTH:
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                                                                   : 756 base pairs
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   other nucleic
/desc = "synth
                                                  double
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synthetic"
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GENERAL INFORMATION:
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                                           REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                         ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S.
REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                          STATE: NY
COUNTRY: US
ZIP: 11553
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                                                                                                                     APPLICATION NUMBER: FILING DATE: 03-JUN CLASSIFICATION: 435
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                            TELEPHONE:
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               TELEFAX:
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 FOR
                                                                                                                                                                                                                                                                                                                       333 EARLE OVINGTON
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CONNOLLY, KEVIN
              516-228-8516
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                                                                                                                                                                                                                                                                          SD
                                                                                                                                                                                  PatentIn Release #1.0, Version
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                               516-228-8484
SEQ ID
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Pred. No. 1.7e-22;
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282

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61 CCTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTGCAGGCCCGCCAGGTGCGCCTGGA 120
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                                                                                                                                                                                                                                                                                                                Length 432;
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Pred. No. 2.3e-19;
0; Mismatches 185;
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APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: d0878579US 1.5STING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin ver. 2.0
       20,015
RR: A55556-3/BIR
                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/09029348 Patent No. 6171827
                         REFERENCE/DOCKET NUMBER: ASTELECOMMUNICATION INFORMATION
                                                         TELEPHONE: (415) 494-8700 TELEFAX: (415) 494-8771 TELEEX: 910 277299 FHT UR INFORMATION FOR SED ID 0. 48: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.3%;
52.8%;
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54.0%;
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ORGANISM: Artificial Sequence
                                                                                                                                                      LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                    Conservative
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Best Local Similarity 52.8
Matches 229; Conservative
         REGISTRATION NUMBER:
                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1608
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                                                                                                                                                                                                                                                                                                                                                      Matches 217;
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                                                                                                                                                                                                                               97 CAGCTCATCAAGAATTTTACAATACTACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGT 156
                                                                                                                                                                                                                                                                       104 CTGGTCCCCAAGGCTTCCCAAGGCTTCCAAGGTCCCCCTGGTGAGCCTGGCGAGCCTGGA 163
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                                                                                                                                                                                               Gaps
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                                                                                                                                                          Length 3181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREEFT: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California
                                                                                                                                                                                           224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                      Score 113.6; DB 1;
Pred. No. 5e-21;
0; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/642,255
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Patent No. 5773249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
                                                                                                                                                        11.1%;
52.5%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROWLAND, Bertram I
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SEQUENCE CHARACTERISTICS:
LENGTH: 3181 base pairs
TYPE: nucleic acid
STRANDENBESS: single
TOPOLOGY: unknown
                                                                                                                                                      Query Match 11.1
Best Local Similarity 52.5
Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                            MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
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                                                                                                              US-08-655-086-1
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                                                                                 421 GCTGGCAAACATGGAAACCGTGGTGAAACTGGTCCTTCTGGTCCTGTTGGTCCTGCTGGT
                                                                                                           GAGAGAGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAA
                                                                                                                                                                     GGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCC
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                                                      ACTGGCAACAAGGACAGAAAGGAGAGAGAGGGGGAGCCTGGACCACCTGGCCCTGCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reeders, Stephen T.
APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRIY APPLICATION DATA:
APPLICATION NUMBER: US/08/494,168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40397/104/BABR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US 08/112,465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 40
TELECOMMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
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ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
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TITLE OF INVENTION: Polynucleotides
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yale University, Office of Cooperative Research
STREET: 246 Church Street
                                                                                                                                      join(2..82, 86..97, 101..4399, 4403..4420, 4424
..4465, 4469..4876, 4880..5101)
                                                                                                                                                                                                                                      Length 5102;
                                                                                                                                                                                                                                                                                            0; Mismatches 200; Indels
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MEDIUM TYPE: Diskette, 3.50 inch, 800K storage
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FILING DATE: 11/30/90
CLASSIFICATION: 424
PRIOR APPLICATION DATA: NO. 5424408 applicable
ATTORNEY/AGENT INFORMATION:
NAME: BAITH, RICHARD S.
REGISTRATION NUMBER: 28180
                                                                                                                                                                                                                                        Score 100; DB 1;
Pred. No. 2.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 28180
REFERENCE/DOCKET NUMBER: 900983/RB
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OPERATING SYSTEM: Macintosh OS7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                        Query Match 9.7%;
Best Local Similarity 52.4%;
                                                                                                                                                                                                                                                                                                  Matches 220; Conservative
                                double
TYPE: nucleic acid
STRANDENESS: double
TYPOLOGY: linear
FRATURE:
NAME/KEY: CDS
LOCATION: join(2..82)
LOCATION: ..4465, 44
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STATE: Connecticut
COUNTRY: U.S.A.
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US-09-167-364-1

Sequence 1, Application US/09167364

; Patent No. 6007980

; GENERAL INFORMATION:
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   FILE REFERENCE: 951263A
                                                                                                                                                                                                                    ; LOCATION: (1)..(1416)
US-08-399-889-1
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                      TYPE: DNA
ORGANISM: Calf
                                                                                                                                                                                                      NAME/KEY: CDS
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Best Local Simi
Matches 228;
                                                                                                                 SEQ ID NO 1
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APPLICANT: Reeders, Stephen T
APPLICANT: Merison, Karen E
APPLICANT: Hudson, Bllly G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.7%; Score 99.6; DB 1; Length 1416;
51.6%; Pred. No. 2e-17;
tive 0; Mismatches 214; Indels 0
                                                                                                                                                                                                                                                                                                                                                                   No. 5424408 known
: No. 5424408 known
ION: No. 5424408e
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                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE: Unknown
DEVELOPMENTAL STAGE: Unknow
TELECOMMUNICATION INFORMATION:
                                           TELEX: 236268
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1416 base pairs
                                                                                                                                             TOPOLOGY: Linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                   CELL TYPE: Whole kidney IMMEDIATE SOURCE: LIBRARY: Bovine lens CDNA
                 TELEPHONE: (212) 972-14
TELEFAX: (212) 370-1622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                    CLONE: KMC15
POSITION IN GENOME: NO.
CHROMOSOME/SEGMENT: NO
PUBLICATION INFORMATION:
                                                                                                                                  Double
                                                                                                               TYPE: Nucleic acid
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Best Local Similarity
                                                                                                                                                                                                                                                    Unknown
                                                                                                                                                                                                                                    Calf
                                                                                                                                                                                                 ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                 STRANDEDNESS:
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US-08-399-889-1
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APPLICANT: Morrison, Karen E
APPLICANT: Morrison, Karen E
APPLICANT: Morson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 951263B
CURRENT APPLICATION NUMBER: US/09/167,364
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: 08/399889
EARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1416;
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CURRENT APPLICATION NUMBER: US/08/399,889B
CURRENT FILING DATE: 1995-03-07
EARLIER APPLICATION NUMBER: 07/621091
EARLIER FILING DATE: 1990-11-30
NUMBER OF SEO ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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343 CCAGGCATGAAAGGGAAGAAGGTAATTCAGGATTTCCAGGACCACCTGGACCTCCAGGG 402
                                                                                                              307 GGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCC 366
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                                                                                                                                                                                         AGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGGACTCCCCGGCCCTCAGGGC
                                                                                                                                                                                                                                                                                                                                               No. 5691197el Macrophage Receptor with a Collagenous Domain and the Polypeptide Chain Encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tryggvason, Karl
APPLICANT: Elomaa, Outi
APPLICANT: Elomaa, Marit
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STREET: 1100 Superior Avenue
STREET: Saite 700
CITY: Cleveland
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MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 70 Kb storable
COMPUTER: IBM PS/2, Model 35 SX
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08392367B Patent No. 5691197
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Word Perfect 5.1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
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Nucleic acid
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CORRESPONDENCE ADDRESS:
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STATE: Ohio
COUNTRY: U.S.A.
ZIP: 44114-2518
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Patent No. 6277558
GENERAL INFORMATION:
APPLICANT INFORMATION:
ALICHA OF INVESTION:
ALICHA OF INVESTION: Aligha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 95-1263-C
CURRENT APPLICATION NUMBER: US/09/439,897
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
                                                                                            5; DB 3; Length 1416; 2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.7%; Score 99.6; DB 4; Length 1416; 51.6%; Pred. No. 2e-17;
                                                                                          Score 99.6; DB 3; Length 1.
Pred. No. 2e-17;
0; Mismatches 214; Indels
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                                                                                            9.7%;
                                                                                          Query Match 9.7
Best Local Similarity 51.6
Matches 228; Conservative
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; LOCATION: (1)..(1416)
US-09-439-897-1
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LENGTH: 1416
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Matches 228;
                                 ; LOCATION: (
US-09-167-364-1
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                                                                                                                 Query Match 9.7%; Score 99.4; DB 1; Length 1868; Best Local Similarity 51.5%; Pred. No. 2.6e-17; Matches 229; Conservative 0; Mismatches 216; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08893467A
Patent No. 6063901
GENERAL INFORMATION:
APPLICANT: Trygvascon, Karl
APPLICANT: Elomaa, Outi
APPLICANT: Kangas, Maarit
TITLE OF INVENTION: An Insolated DNA Sequence For a
Patent No. 6063901
TITLE OF INVENTION: No. 6063901el Macrophage Receptor with
TITLE OF INVENTION: a Collagenous Domain and the
TITLE OF INVENTION: Such a Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fay, Sharpe, Beall, Fagan,
Minnich & McKee
STRANDEDNESS: Single
TOPCLOGY: Linear
MOLECULE TYPE: Nucleotide-genomic DNA
HYPOTHETICAL: No. 5691197 relevant
ANTI-SENSE: No. 5691197 relevant
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 720 Kb storable
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OPERATING SYSTEM:
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                                                                   ; ANTI-SENSE:
US-08-392-367B-1
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1081 CCAGGCCCTCAAGGTGCACCAGGACTTTCAGGTGCCAAGGGTGAGCCAGGACGCACTGGT 1140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 GGTGAGAGGCCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAAGGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGCCCTCAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124 CAAGGICCACGGGCCCCAGGGGICCAAGAGGIGACAGAGGAICCCAGGGACCCCTGGC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 CCAACTGGCAACAAGGGACAGAAAGGAGAGAAGGGGGGAGCCTGGACCTGGCCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCCATGCCAGGCCCCCAAGGGCCCCCCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               424 GGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGACCT
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Patent No. 5773248
GENERAL INFORMATION:
APPLICANT: Breaton, Richard G.
APPLICANT: Maye, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 9.7%; Score 99.4; DB 3; Best Local Similarity 51.5%; Pred. No. 2.6e-17; Matches 229; Conservative 0; Mismatches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Linear
MOLECULE TYPE: Nuclectide-genomic DNA
HYPOTHETICAL: No. 6063901 relevant
US-08-893-467A-1
                       US/08/893,467A
                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
REFERENCE/DOCKET NUMBER: TRV 2 00)
TELECOMMUNICATION INFORMATION:
TELEPAX: (216) 241-166
TELEPAX: (216) 241-166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  544 CCTCCTGGCCCATCAGGAGCGGTGG 568
                                                                                                                                                                                                                                                                                                                                                   1868 base pairs
                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid
EDNESS: Single
                                                                         CLASSIFICATION: 435
CURRENT APPLICATION DA APPLICATION NUMBER:
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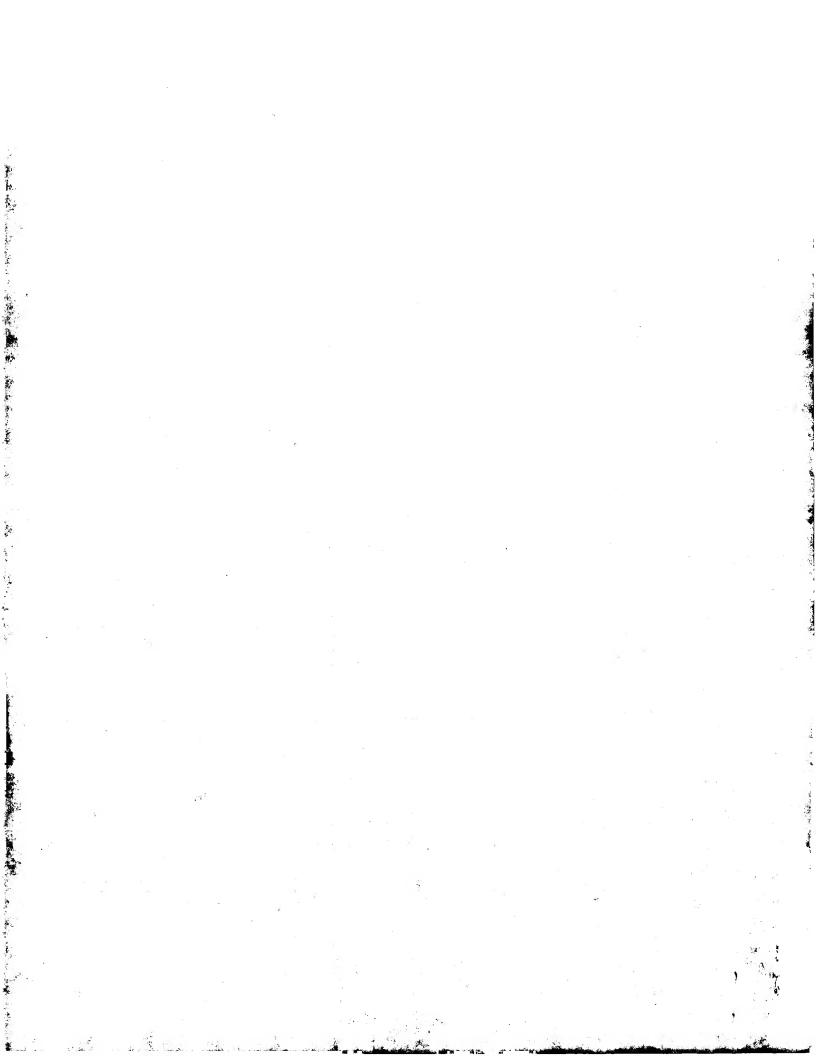
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6127523
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; LOCATION:
US-09-073-663-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTGAGAGGCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGCGCCAAAGGATCT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 AAAGGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           824 GCGCCTGGGAAAGCGGGTGACCGAGGCGAGGGGCCCAGAAGGGTTCCGCGGGCCCCAAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGGTGCCTGGACCT 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 99.4; DB 1; Length 2:
Pred. No. 3e-17;
0; Mismatches 216; Indels
                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                     FILING DATE: 13-NOV-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                8389-030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1004 GAGGCTGGTCGCAACGGTGCTCCGG 1028
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US-09-073-663-11
; Sequence 11, Application US/09073663
                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFRENCE/CDCKET NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
                                                                                                                                                                                                                                                                                                           TELEFAX: 415-854-3694
TELEX: 6644 PENNE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.5<sup>3</sup>
Matches 229; Conservative
                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47..2098
                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: unknown MOLECULE TYPE: CDNA
                 New York
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
                              USA
                                              10036
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US-08-555-669-11
                              COUNTRY:
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124 CAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGC 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              704 GCCCTCCCGGCCAGCGTGGGGCTTCCAGGGCCCCCGGGGATTACGAGGACTGCCAGGGCCA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        764 CTCGGGCCCCCTGGGGACCGGGGTCCCATTGGGTTCCGAGGGCCGCCTGGGATCCCAGGA 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            644 GAGCAGGGGAAGTCGGCAAGGACGCGAGAAGGTGACCCTGGCCCCCCGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GGTGAGAGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCGAAAGGATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 CCCAGTGGGGACCCAGGCCCCCCGGGCCCACCAGGCAAAGAGGGGACTCCCCGGCCCTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.7%; Score 99.4; DB 3; Length 2543; Best Local Similarity 51.5%; Pred. No. 3e-17; Matches 229; Conservative 0; Mismatches 216; Indels 0
                    APPLICANT: Brewton, Richard G.
PAPLICANT: Mayne, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5913D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 8.1
SOFTWARE: Microsoft WORD for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,663
                                                                                                                                                        ADDRESSEE: McGregor & Adler, LLP STREET: 8011 Candle Lane CITY: Houston CITY: Houston COUNTRY: USA ZIP: 77071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ 1D NO: 11:
SEGUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: unknown
                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47..2098
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GENERAL INFORMATION:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 GAGAGCGTGGCGGCAAAGGATCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCC 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 341 CTGGGAAGCCCGGCCCTCAGGGCCCCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGCA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401 AAGAGGGACTCCCCGGCCCTCAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTG 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55 GTGATTATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                461 GGGAGCCTGGGGTGCCTGGACCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGC 520
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
9.5%; Score 97.6; DB 4; Length 4359;
Best Local Similarity 52.3%; Pred. No. 1.2e-16;
Matches 272; Conservative 0; Mismatches 234; Indels 14
                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6426186 331365 (1553795CB1)
US-09-484-970B-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 CAGGCCCCAAGGGCCCCCCGGCCCTCTGGCCCATCAGG 560
                                               RESULT 15
US-09-484-970B-4
; Sequence 4, Application US/09484970B
; Patent No. 6426186
; GENERAL INFORMATION:
; APPLICANT: Jones, Karen A.;
; APPLICANT: Volkmuth, Wayne;
; APPLICANT: Walker, Michael G.;
; TITLE OF INVENTION: BOONE REMODELING GENES;
; FILE REFERENCE: PB-0014 US.;
CURRENT FILING DATE: 2000-01-18
; WUMBER OF SEQ ID DATE: 2000-11-8
; SEQ ID NOS: 172
; SOFTWARE: PERL PROGRAM
; TENLY NOS: 172
                   1004 GAGGCTGGTCGCAACGGTGCTCCGG 1028
544 CCTCCTGGCCCATCAGGAGCGGTGG 568
                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                 LENGTH: 4359
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completed: March 21, 2003, 08:25:53 le: 48.1652 secs

Search co



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March 21, 2003, 01:57:56 ; Search time 156.339 Seconds
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  5089.177 Million cell updates/sec
                                                                                                                                                                                                                                            1 atgcaacaagatttgatgag.........
version 5.1.4_p5_4578 - 2003 Compugen Ltd.
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                                                                                                                                                                                     US-09-763-712A-1_COPY_670_1695
1026
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Maximum Match 1008
Listing first 45 summaries
                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                  IDENTITY_NUC Gapop 10.0 , Gapext 1.0
GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                            Sequence:
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55: 76: 76: 10: 11: 12: 14:

Published\_Applications\_NA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

, Description	Sequence 198, App Sequence 3946, App Sequence 57, Appl Sequence 57, Appl Sequence 64, Appl Sequence 64, Appl Sequence 3947, App Sequence 206, App Sequence 206, App Sequence 206, App Sequence 22, Appl Sequence 33, Appl Sequence 25, Appl Sequence 25, Appl Sequence 25, Appl Sequence 26, Appl Sequence 26, Appl Sequence 786, Appl Sequence 762, Appl Sequence 762, Appl
SUMMARIES	US-09-745-763-198 US-09-954-456-782 US-09-924-40-57 US-09-922-600A-57 US-09-925-302-64 US-09-925-302-64 US-09-925-302-64 US-09-925-302-64 US-09-925-309-206 US-09-925-299-206 US-10-044-090-32 US-10-044-090-32 US-09-954-631-961 US-09-954-451-961 US-09-954-456-786 US-09-919-497-6 US-09-919-497-6 US-09-919-407-6 US-09-919-407-6 US-09-919-407-6
DB	
% Query Match Length DB	5930 6728 11338 11338 11338 11338 11338 11338 11338 1145 1145 1145 1146 1146
% Query Match	0.00 0.00 0.00 0.00 0.00 0.00 0.00 0.0
Score	1024.4 1024.4 111111110.6 1100.6 1100.7 1007.2 1007.2 1007.2 1007.2 1006.8 1005.2 1005.2
Result	100 8 4 5 9 7 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1

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                                                                 1; Indels
                                                 Score 1024.4; DB ]
Pred. No. 1.7e-271;
                                                                 0; Mismatches
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 198:
                                               99.88;
                                                        Best Local Simitatiny Matches 1025; Conservative
                               US-09-745-763-198
                                                 Query Match
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for Identifying Anti-Cancer Therapeutic Agents Using
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122 TACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                TITLE REFERENCE (89290-76

CURRENT APPLICATION NUMBER: US/09/954,456

CURRENT FILING DATE: 2001-09-18

PRIOR PILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-18

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

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PRIOR FILING DATE: 2000-09-26

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PRIOR PRILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR PRILING DATE: 2000-09-26

PRIOR PRILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,840

PRIOR PRILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: US/60/235,840

PRIOR PRILING DATE: 2000-09-27
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                                                                                                                                                                                                                                                                          Sequence 782, Application US/09954456
Patent No. US20020115057A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Process
TITLE OF INVENTION: Sets
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Young, Paul
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Matches 237; Conserv
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US-09-954-456-782
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LENGTH: 6728
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SOFTWARE: JPatent
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MAME/KEY: CDS
LOCATION: 476..964
NAME/KEY: 3'UTR
LOCATION: 965..1133
NAME/KEY: POLYA_Signal
LOCATION: 1101..1106
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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NAME/KEY: 5'UTR
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AGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGGAGCCTGGGGTGCCTGGAC 481
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                                                             CTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCCCG
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Occkley, Joseph G.
APPLICANT: Occkley, Joseph G.
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer:
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PALENTIN Ver. 2.1
SEQ ID NO 3946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6728;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.8%; Score 111; DB 10; Length 6
Best Local Similarity 53.0%; Pred. No. 3.7e-20;
Matches 237; Conservative 0; Mismatches 210; Indels
                                                                                                                                               1141 GTCCTCCTGGCTTCCCTGGTGCTGTTG 1167
                                                                                                                              GCCCTCCTGGCCCATCAGGAGCGGTGG 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                             RESULT 3
US-09-880-107-3946
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGTCCCCCCGG-----AGAGCGTGGCGGCAAAGGATCTAAAGGCTCCCAGGGCCC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 CAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGTGGGGACCCAGG 380
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                                                                        APPLICANT: Bejanin, Stephane
APPLICANT: Bejanin, Stephane
TILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.022.REG
CURRENT APPLICATION NUMBER: US/09/924,340
CURRENT FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-59
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR APPLICATION NUMBER: US 60/293,574
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Sequence 57, Application US/09924340 Publication No. US20030027248A1 GENERAL INFORMATION:
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289 TGGCCCACCTGGCCCTCAAGCAGAAGGCCAAGGAATCGAGGCCCATCAGGCCT 348
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                                                                                     321 CAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGTGGGGACCCAGG
                                                                                                                                                                       441 GGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGACCTCGGGGACTGCCAGGCTT
                                                                                                                                                                                                                                                                                                                501 GCCTGGGGTACCAGGCATGCCAGGCCCCAAGGGCCCCCCGGGCCCTTCTGGCCCATCAGG
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APPLICANT: Rosen et al.
ITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 10.7%; Score 109.4; DB 10; Best Local Similarity 54.4%; Pred. No. 6.2e-20; Matches 240; Conservative 1; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING BATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR FLING DATE: 1999-03-12
PRIOR PLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: n equals a,t,g, or c NAME/KEY: misc feature LOCATION: (2683)
COTHER INFORMATION: n equals a,t,g, or c US-09-925-302-64
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NAME/KEY: misc feature
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LOCATION: (2653)
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ORGANISM: Homo sapiens
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                 501 GCCTGGGGTACCAGGCATGCCAGGCCCCAAGGGCCCCCCCGGGCCCTCCTGGCCATCAGG
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US-09-992-600A-57

US-09-992-600A-57

Sequence 57, Application US/09992600A

Publication No. US20030027161A1

GENERAL INFORMATION:
APPLICANT: Benjamin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91 US4.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A

CURRENT RILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PRICATION NUMBER: US 60/305,456
PRIOR PRICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/203,574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: US 60/293,574

PRIOR FILING DATE: 2001-06-15
PRIOR PRICATION NUMBER: US 60/293,574

SEQ ID NO 57

LEMCTH: 1133

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LEMCTH: 1133
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Pred. No. 1.8e-20;
0; Mismatches 229;
                                                                                                  561 AGCGGTGGTGCCCTGGCCGTGCAG 585
                                                                                                                                         589 TGAACCTGGTGCCATGGGACCCCAG 613
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ilarity 52.9%;
Conservative (
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ORGANISM: Homo sapiens
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LOCATION: 1101..1106
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1118..1133
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Best Local Similarity
Matches 267; Conserv
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FEATURE:
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US-09-992-600A-57
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FEATURE:
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                                                                                                                                        Sequence 3947
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                                                                                                                                                                                                                                                 Sequence 42, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 2192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.4%; Score 107.2; DB 10; larity 53.5%; Pred. No. 2.2e-19; Conservative 0; Mismatches 228;
                                                                                                                                                                                   GGCCCTCCTGGCCCATCAGGA 561
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US-09-925-301-42
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                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: HORDE, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Lodg, Inc.
ITILE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028 WO
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-14
SOFTWARE: PATENTON NUMBER: US 60/237,054
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VEY: 2.1
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OTHER INFORMATION: Genbank Accession No. US20020142981A1 274616
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Pred. No. 4e-19;
0; Mismatches 235; Indels
                                                                                                                   1109 GACTTCAGCTTCCTGCCCAGCCACCTCAAGA 1140
                                                                           GGAGGACAATGGCTGCCCGCCTCACTGGAAGA 637
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; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3947
                                                                                                                                                                                                                                                                              Sequence 3947, Application US/09880107 Patent No. US20020142981A1
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10.4%;
Best Local Similarity 51.3%;
Matches 248; Conservative (
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952 TGGTAACGCTGGTCGTGGTCCCGCCCGTCCCCGTGGTGAACGCGTCTTCCAGGCCT 1011
1072 TGCTGCTGCCTTCCCGGCGTTGCTGGGGCTCCCGGGCCTCCCTGGACCCCGCGGTATTCC 1131
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                                                                                                                                                                                                                                                            Sequence 206, Application US/09925299
; Sequence 206, Application US/09925299
; Patent No. US200205557A1
; GENERAL INFORMATION:
; APPLICANT: ROSen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR PAPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 1909-03-08
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PAtentIN Ver. 2.0
; SEQ ID NO 206
; LENGTH: 5145
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Best Local Similarity 51.3%; Pred. No. 4e-19;
Matches 248; Conservative 0; Mismatches 235;
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OTHER INFORMATION: n equals
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                                                                                                                                                                                                           Sequence 206, Application US/09925299
Publication No. US2003004061789
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 12099-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (5126)

OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc_feature
LOCATION: (5143)

OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-206
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                                                                                            1189 AGC 1191
                                                                600 GGC 602
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US-09-925-299-206
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LENGTH: 5145
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APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yorgming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes of the Respence: DEX-0269
CURRENT APPLICATION NUMBER: US/10/001,887
CURRENT PILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: 60/252,563
PRIOR FILING DATE: 2000-11-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               540 CGGCCCTCCTGGCCCATCAGGAGCGGTGGTGCCCTTGGCCGTGCAGAATGAGCCAAACCCC 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.4%; Score 106.8; DB 9; Best Local Similarity 52.9%; Pred. No. 4.4e-19; Matches 256; Conservative 0; Mismatches 222;
                                                                                            Sequence 33, Application US/10001887 Patent No. US20020155464A1
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 137
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                         Macina, Roberto
                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Salceda, Susana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; ORGANISM: Homo sapien
US-10-001-887-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2083 CGCA 2086
1522 AGC 1524
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US-09-954-531-961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 33
LENGTH: 4908
                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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                                                                                                                                                                                                                                                                              Sequence 22. Application US/10044090
Sequence 22. Application US/10044090
Patent No. US20020137081A1
September 1. INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILE OF DID NOS: 850
SOFTWARE: PERL PROGRAM
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                                        1072 TGCTGCTGGCCTTCCCGGCGTTGCTGGGGCTCCCGGCCTCCCTGGACCCCGCGGTATTCC 1131
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                                                                                      540 CGGCCCTCCTGGCCCATCAGGAGCGGTGCTCCCTGGCCCTGCAGAATGAGCCAACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10.4%; Score 107; DB 12; Length 5432; 51.3%; Pred. No. 4.1e-19; tive 0; Mismatches 235; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 51.33
Matches 248; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
FEATURE:
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1192 AGC 1194
                                                                                                                                                                   GGC 602
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LENGTH: 5432
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US-09-954-456-786

; Sequence 786, Application US/09954456
; Sequence 786, Application US/09954456
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Pecess for Identifying Anti-Cancer Therapeutic Agents Using C; TITLE OF INVENTION: Sets
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTG 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 106; DB 10;
Pred. No. 5.1e-19;
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      PRIOR APPLICATION NUMBER: 2001-09-27
PRIOR APPLICATION NUMBER: US/60/236.033
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US/60/236.032
PRIOR APPLICATION NUMBER: US/60/236.028
PRIOR PLILING DATE: 2000-09-28
PRIOR FILING DATE: 2000-09-28
NUMBER OF FILING DATE: 2000-09-28
SOFTWARE: PATENTIN NUMBER: US/60/236.028
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 255
LENGTH: 2542
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CURRENT APPLICATION NUMBER: US/09/954,456

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: US/60/23,617

PRIOR PELING DATE: 2000-09-18

PRIOR PELING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-25

PRIOR PELING DATE: 2000-09-25

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR FILING DATE: 2000-09-25

PRIOR PILLING DATE: 2000-09-25

PRIOR PILLING DATE: 2000-09-25

PRIOR PILLING DATE: 2000-09-25

PRIOR PAPPLICATION NUMBER: US/60/235,134

PRIOR PAPPLICATION NUMBER: US/60/235,637
CURRENT APPLICATION NUMBER: US/09/964,824A CURRENT FILING DATE: 2001-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 10.3%;
Best Local Similarity 52.1%;
Matches 236; Conservative
                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-09-964-824A-255
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                      TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancer TITLE OF INVENTION: Gene Sets
TITLE OF INVENTION: Gene Sets
FILE OF INVENTION: Gene Sets
FILE OF INVENTION: Gene Sets
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR PILING DATE: 2000-09-18
PRIOR PELING DATE: 2000-09-20
PRIOR PELING DATE: 2000-09-20
PRIOR PELING DATE: 2000-09-20
PRIOR PELING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR PILING DATE: 2000-09-22
PRIOR PELING DATE: 2000-09-22
PRIOR PILING DATE: 2000-09-22
PRIOR PELING DATE: 2000-09-22
PRIOR FILING DATE: 2000-09-22
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APPLICANT: Horrigan, Stephen
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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Pred. No. 5.1e-19;
0; Mismatches 217; Indels
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   Application US/09954531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.3%;
52.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-531-961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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                                                PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SEQ ID NO 786
LENGTH: 5416
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
                                                                                                                                                                                                                                                                                                                                    Query Match 10.3%;
Best Local Similarity 51.1%;
Matches 247; Conservative
                                                                                                                                                                                                                                                                 TYPE: DNA
CORGANISM: Homo sapiens
US-09-954-456-786
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Search complèted: March 21, 2003, 08:22:40 Job time : 175.339 secs

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5.1.4_p5_4578 Compugen Ltd.	Search time 1346.02 Seconds (without alignments) 12344.923 Million cell updates/sec	ta 1	sən	rs: 32308132						results predicted by chance to have a to the score of the result being printed, of the total score distribution.	Description	BC000162 Mus muscu BQ713873 ACENCOURT BQ674807 ACENCOURT AL56843 AL568743 BI456109 603172765 BE910803 601661855
GenCore version 5 Copyright (c) 1993 - 2003 Co	OM nucleic - nucleic search, using sw model Run on: March 21, 2003, 01:34:06; Searce (with	2A-1_COPY_670_169 atttgatgag	Gapop 10.0 , Gapext 1.0 Searched: 16154066 seqs, 8097743376 residue	Total number of hits satisfying chosen parameters Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : EST:*  1: em_estba:* 2: em_esthum:* 3: em_estlun:* 4: em_estlu:* 5: em_estlu:* 6: em_estlu:* 7: em_estlo:* 9: gb_estl:* 10: qb_estl:*		14: 9D_estb:* 15: em_estfun:* 16: em_estcon:* 17: 9D_gss:* 18: em_gss_hum:* 19: em_gss_lun:* 20: em_gss_pln:* 21: em_gss_pln:*		al s	* Result Query No. Score Match Length DB ID	1 800.4 78.0 3305 11 BCC09162 2 556.4 54.2 861 14 BQ713873 3 525.4 51.2 668 14 BQ74807 c 4 475.4 46.3 967 9 AL568743 5 462.6 45.1 906 13 B1456109 6 445.6 43.4 580 12 BE910803

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BQ713873
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KEYWORDS
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                                                                Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: h Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
              Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.
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                                                                                                                                                  This clone has the following problem: incomplete processing.
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               × ; ;
                                                                                                                                                                                                                               /clone="IMAGE:2811487"
/tissue_type="Wammary tumor. Vold, gross tissue."
/clone_lib="NoI_CGAP_Mam5"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6"
757 c 760 g 757 t
                                                                                                                                                                                                                                                                                                                                                       Score 800.4;
Pred. No. 2.4
Contact: amg@bcm.tmc.edu
dunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
                                                                                                                                                            Location/Qualifiers
1. .3305
                                                                                                                                                                                                                                                                                                                                                       78.0%;
86.3%;
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/lab_host="OH10B" (phage-resistant)"
/nab_host="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ713873 861 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8482828 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6306240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 80).

NIH-WGC http://mgc.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
2195
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.inh.gov.
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortlum (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can http://image.llnl.gov
Dlate: LiAM13721 row: n column: 01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2136 GACGGGTCACCTGTTGATTACAAAAACTGGAAAAGCTGGACAACCAGATAACTGGGGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                     2196 GGCCATGGGCCAGGAGAAGACTGTGCTTGATTTACGCAGGACAGTGGAATGACTTC
                                                                                                                                                                                                                                                                                   GATGGGACATCTCCAGACTACAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCAT
                                                                                                                                                                                                                                                                                                                                                                               GGCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTC
                                                                                                                                                                                                               Length 861;
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                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6306240"
/clone_lib="NIH_MGC_129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 598.
Location/Qualifiers
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253 c 239 g
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BQ713873
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/clone="IndexColling"
/clone="IndexColling"
/clone_lib="NIH_MGC_102"
/clone_lib="NIH_MGC_102"
/tissue_type="epidermoid carcinoma, cell line"
/tissue_type="epidermoid carcinoma, cell line"
/tissue_type="epidermoid line"
/tissue_type="epidermoid line"
/note="Organ: salivary gland; Vector: porB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAho! sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                                                      Email: cgapbs-remail.inth.gov
Tissue Procurement: ATC
CDNA Library Preparation. Rubin Laboratory
cDNA Library Preparation. Rubin Laboratory
cDNA Library Preparation. Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLCM2377 row: c column: 09
High quality sequence stop: 656.
Location/Qualifiers
I. 668
//ob_refe"taxon:9666"
//db_refe"taxon:9666"
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCCCGGCCCTGGCCCATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 525.4; DB 14; Length 668;
Pred. No. 3e-114;
); Mismatches 1; Indels 0;
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99.8%;
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Best Local Similarity 99.84
Matches 526; Conservative
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AGENCOURT_8035172 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6212672
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 668)
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                                                                                                   74 AGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATACTACAAGGTCCAC 133
                                                                                                                                                               CGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCAACTGGCA 193
                 Gaps
                                                           TGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATTATGGAAGAAATGA 73
                                                                                                                                                                                                                                                                                                  ACAAGGGACAGAAAGGAGAGAGAGGGGGAGCCTGGACCACCGGCCCTGCGGGTGAGAGG
                                                                                                                                                                                                                                                   194 ACAAGGGACAGAAAGGAGAGAGAGGGAGGCCTGGTCCACCTGGCCCTGCGGGTGAGAGGG
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               Indels
 Pred. No. 1.4e-121;
; Mismatches 132;
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82.88;
               647; Conservative
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BQ674807
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TITLE
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                                                                                                                                          RESULT 5
BI456109
                                                                                                                                                                                                                    ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded CDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Freque Liang Life Technologies. Contact: Freque Liang Life Technologies, and Amaryland 20850, USA Fax: (1) 301 610 8371 Email: http://fulllength.invitrogen.com"
                                             AL568743 LTI_FL002_PL1 Homo sapiens cDNA clone CSODE005xH04 3 prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 967)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Unpublished (2001)
Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 9106 EVRX cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    686 AGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCATAAACACTAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.3%; Score 475.4; DB 9; 96.7%; Pred. No. 2.6e-102;
                                                                                                                                                                                                                                                                                                                                        1. .967
/organism="Homo sapiens"
/db_xxef="Laxon:9606"
/clone="CSODE005YH04"
/clone_lb="LTL FL002_PL1"
/lab_host="DH109"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                             AL568743
AL568743.1 GI:12923387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504; Conservative
                                                                             mRNA sequence.
                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
                                                                                                                                          human.
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                RESULT 4
AL568743/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Loca
Matches
                                                           DEFINITION
                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
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                                                                                                                                                       ORGANISM
                                                                                          ACCESSION
                                                                                                        VERSION
KEYWORDS
SOURCE
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone=Inb="NoI_C6AP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/dev_stage="7 months"
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pcMV-SPORT6; Site_1: SalI;
/note="Organ: mammary; Vector: pcMV-SPORT6; Site_1: SalI;
/note="Organ: cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 906)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.inh.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                         906 bp mRNA linear EST 21-AUG-2001
603172765F1 NCI_CGAP_Mam5 Mus musculus CDNA clone IMAGE:5251888 5',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGCAACAAGATTTGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATT 60
Query Match 45.1%; Score 462.6; DB 13; Length 906; Best Local Similarity 81.7%; Pred. No. 2.8e-99; Matches 597; Conservative 0; Mismatches 124; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM1636 row: b column: 17 High quality sequence stop: 730. Location/Qualifiers
                                                                                986 TTTGCGAAAAAGACAGGGAGACAGTACTGTCATCTGCATTA 1026
                                                                                                          256 g
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BI456109.1 GI:15246765
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Matches 496; Conservative
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AW958053
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus , Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 580) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                              480
                                                                                                                                                           009
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                                         GGCCCCAGTGGGGACCCAGGCCCCCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGGCCCT 420
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                            TCTAAAGGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAG 360
                                                                                                                                                                                                                                                                                                                                                                            ACTATTTTCAGTTG----AGAAAGAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACA 712
363 GCGGGTGAGAGGGGCACAATTGGACCAGTCGGCCCTCCTGGAGAGCGTGGCAGCAAAGGA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incytte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                  GGCCCTCCTGGCCCATCAGGAGGGTGGTGCCCCTGGCCCTGCAGAATGAGCCAACCCCG
                                                                                                                                                                                                                                                                                                                   GCACCGGAGGACAATGGC - - TGCCCGCCTCACTGGAAGAACTTCACA - - - GACAAATGCT
                                                                                                                                           421 CAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGA
                                                                                                                                                                                                                                                                                                                                  found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9128 row: m column: 13
High quality sequence stop: 580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="IMAGE:3962292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
1. .580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="FVB/N"
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AATTTTCCAAT 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
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AUTHORS
TITLE
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AW958053 552 bp mRNA linear EST 01-JUN-2000 EST370123 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence. AW958053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000) contact: John Quackenbush
/dev_stage="10 months, virgin"
/lab_nost="HHIDB"
//lab_nost="HHIDB"
//note="Organ mammary; Vector: pCMV-SPORT6; Site_1: Sal
Site_2: NotI; Cloned unidirectionally. Primer: Oligo o
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                          409
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                                                                                                                                                                                                                                                     Gaps
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and
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                                                                                                                                                                                                                                                                                                                                                                                                               481 ATACCGTGGGGAGAAAGCCATTGGATCGGCCTCACAGACTCAGAACAGGAAAT
                                                                                                                                                                                                                                                                                                                       350 CCGGCCCTCAGGGCCCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.10 TCCCCGGCCCTCAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACAAGTCTTCACATCTTGTTTTCATAAACACTAGAGAACAGCAATGGATAAAAAAC
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0
                                                                                                                                                                                                           Length 580;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Bu
Bukaryota; Butheria: Primates; Catarrhini; Hominidae; H
1 (bases 1 to 552)
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R.,
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. a
Quackenbush, J.
                                                                                                                                                                                                      Score 445.6; DB 12; Length
Pred. No. 2.6e-95;
); Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGAAGTGGCTGGATGGGACATCTCCAGACTACAAAATTG 869
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85.5%;
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BASE COUNT ORIGIN

FEATURES

Matches

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61

754 181 814

874 301 934 993

421

361

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EST 21-AUG-2002
                                                                                                                                                                                                                /Clone_Inbace: IMAGE: 3484163."
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev.stage="Tumoths"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                    DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/Link at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196 AAGGGACAGAAAGGAGAAGGGGGAGCCTGGACCACCTGGCCCTGGGGGTGAGAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 CCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAAGGCTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 ACAATTGGACCAGTCGGCCCTCCTGGAGAGCGTGGCAGCAAAGGATCCAAAGGCTCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 GGCCCCAAAGGCTCCCGTGGTTCCCCTGGG-AAGCCCGGCCCTCAGGGCCCCAGTGGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       555 ATCAGGAGCGGTGCTCCTTGGCCCTGCAGAATGAGCCAACCCCGGCACCGGAGGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         615 TGGCTGCCCGCCTCACTGGAAGAACTTCACAAAATGCTACTATTTTTCAGTTGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCAT
     cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACACTAGAGGAACAGCAATGGATAAAAAAAACAGATGGTAGGGAGAGA 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 415.8; DB 10;
Pred. No. 3.2e-88;
0; Mismatches 87;
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                                                                                        Plate: LLAM8516 row: k column: 12
High quality sequence stop: 551.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                               105
                                                                                                                                                            /organism="Mus musculus"/strain="C57BL/6J"/db_xref="taxon:10090"
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Best Local Similarity 84.8%;
Matches 501; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 601)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                 693
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National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                        Length 552;
                                                                                                                                                                                                                                                                                                                             Indels
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, 18712 Medical Center Dr., Rockville, MD 20850, Fax: 301 838 9208 Email: johnq@tigr.org Plate: 115 Seq primer: Reverse.
                                                                                                                         Location/Qualifiers
1..552
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="WAGE resequences, MAGE"
/note="Vector: pBluesoriptSkm"
a 112 c 143 g 121 t
                                                                                                                                                                                                                                                                                          DB 10;
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Pred. No. 2.5e-93;
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VERSION KEYWORDS SOURCE ORGANISM

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REFERENCE AUTHORS

DEFINITION

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773 CANGGCCCTCCTGGCTT-CAGGGACTACAGGGCACTGTGGGTGAGCCTGGAGTACCTGGA
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KEYWORDS
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/db_xref="taxon:10090"
/clone="InAGE:6313500"
/clone="InBAGE:6313500"
/clone="InB-nulum MGC_129"
/lab_host="DH10B (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
/note="Organ: olfactory epithelium; Vector: Note: this
AGENCOURT_8763247 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313500
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                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 957)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                 CDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov.rl column: 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39.3%; Score 403.4; DB 14;
86.2%; Pred. No. 3.3e-85;
ive 0; Mismatches 72;
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Location/Qualifiers
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                                                 BQ955927.1 GI:22371405
                  mRNA sequence.
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Best Local Similarity 86.2
Matches 481; Conservative
                                                                                     house mouse.
Mus musculus
                      5', MKNA
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DEFINITION
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AUTHORS
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Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramuco,K., Ishi,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Ishi,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki, J., Shibata,K., Shinaqawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y. et al. 2001)

NI RIKBN Mouse ESTS (Arakawa,T., et al. 2001)

On Jul 6, 2000 this sequence version replaced gi:8940810.

Contact: Yoshinde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)

The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-resegac.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
Carninci,P. Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazak,Y., Hayatsu,N., and Hayashizak,Y.
'M., Konno,H., Okazak,Y., Hayatsu,N., and Hayashizak,Y.
'M., Konno,H., Okazak,Y., Hayatsu,M. and Hayashizak,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000)
(11), 1757-1771 (2000)
'Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA
DB248064 RIKEN full-length enriched, 7 days neonate cerebellum Musmusculus CDNA clone A730023E20 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                     BB248064.2 GI:16355610
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source

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Chorovaede—"fetal and adult"

//ab_host-"DH108 (Life Technologies) (TI phage resistant)"

//ab_host-"Under eye, Vector: pr713-pac (Pharmacla) with a modified polylinker; Site_1: ECOR I; Site_2: Not I;

UI-E-EJO is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT773-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contenins a library tag sequence that is located between the Not I site and the (dT)18 that is located between the Not I site and the (dT)18 that is located between the Not I site and the ATSCCCCAT; optic nerve, CCATAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene biscovery in the Visual System, supported by National Eye Institute (NEI).

TAG_LIB-UI-E-EJO

TAG_STGCCATATAGTG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contect: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
7e1: 319 319 358 8250
Fax: 319 319 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: M13 Forward
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 500)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCA 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 AGGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UI-E-EJO-ahq-c-05-0-UI.s2 UI-E-EJO Homo sapiens cDNA clone UI-E-EJO-ahq-c-05-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 351.4; DB 14; Length
Pred. No. 5.9e-73;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="UI-E-EJ0-ahq-c-05-0-UI"
/clone_lib="UI-E-EJ0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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123 c 89 g
                                                                                                       BM676508.1 GI:18986404
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99.7%;
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                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                        human.
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Best Local S
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ORIGIN
      DEFINITION
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                                                                        ACCESSION
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                          Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" of the contributed of the contributed of the contributed with a primer [5" of the contributed with a primer [5] of the contributed with a primer [5" of the contributed with a primer [5] of the contributed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CCCCAGCATCAGAGGTCAACGGATGTCCGCCTCACTGGAAGAACTTCACAGATAAATGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTATITITCAGIIGAGAAAGAAAITITIGAGGAIGCAAAGCIIITCIGIGAAGACAAGT 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTCATGGCCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACG 955
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                                                                                                                                                                                            /tissue_type="cerebellum"
/dev_stage="7 days neonate"
/lab_host="DH10B"
/note="site1: Sall; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 3.4e-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
   1. .638
/organism="Mus musculus"
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                                                                    /db_xref="taxon:10090"
/clone="A730023E20"
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84.5%;
                                                                                                                                                                    cerebellum"
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134 c
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Best Local Similarity
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first-strand crystals a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGATCAAGA; lens, CGATTAGCGA, eye anterior segment, AATGCGCAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Chorold, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
         vector. The oligonucleotide used to prime the synthesis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I toases 1 to 808)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BQ771366 UI-M-FIO-byu-g-09-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone IMAGE:5702432 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCGGCCTCACAGACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTCCAG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGGTCATGGCCATGGGCCAGGAG 916
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                                                                                                                                                                                                                                                                                                                                                                                   Length 507;
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                                                                                                                                                                                                                                                                       34.1%; Score 350; DB 14;
100.0%; Pred. No. 1.3e-72;
ive 0; Mismatches 0;
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1. .808
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                                                                                                                                                                                                                                                                                                                   Matches 350; Conservative
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BQ771366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.E.E.J.-ahq-c-05-0-UI.rl UI-E-EJO mRNA linear EST 28-FEB-2002
UI-E-EJO-ahq-c-05-0-UI.rl UI-E-EJO Homo sapiens cDNA clone
BN713891
BM713891.1 GI:19027149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Corgan: eye; Vector: pTT73 Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA Synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-pac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mscares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 507)

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  451 Eckstein — _____ Hodical Research Building Iowa City, IA 52242, USA Tel: 319 335 8260
Fax: 319 335 9565
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853
                                                                                            854 CAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGCCCATGGGCCAG 913
                                                                                                                                                                                                      255
                                                                                                                                                                                                                                                                    eye anterior segment,
                                                                                                                                                                                 GAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGGAACGATTTCCAATGTGAAGACG
                                                                  GGATCGGCCTCACAGACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTC
                                                                                                                                                                                                                                                                                                                                 TCAATAACTTCATTGGGAAAAAGACAGGGACACTACTGTCATCTGCATTA 1026
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Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-E-EJO-ahq-c-05-0-UI"
/clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
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Location/Qualifiers
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SOURCE
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BM713891
LOCUS
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TITLE
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EST 26-JUL-2002

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is Adams, M.D., Kerlavage, A.R., Fletschmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O.J., Sutton, G., Blake, J.A., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fritzhugh, W.M., Fritchman, J.L., Gocahagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. J.T., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Beng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olssen, H., Raymond, L., Weity, P.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, W.R., Rosen, C.A., Haseltine, W.A., Fields, C., Freser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of CDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
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For clone availability, additional sequence and expression

For clone availability, additional sequence and expression

Information related to this EST, please check the TIGR Human Gene

Index (http://www.tigr.org/tdb/hgi/hgi.html)

Seq primer: M13 Reverse.

Location/Qualifiers
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/db_xref="ATCC (inhost):115883"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="Apcre endothelial cells, TNF alpha-treated"
/call_type="endothelial cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: aorta; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                873 AGCTGGACAGCCGGAT -- AACTGGGGTCATGGCCATGGG 909
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Pred. No. 2.1e-63;
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                                                     AUTHORS
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                                 /clone_inb="Indaga" /
/clone_inb="Indaga" /
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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85.1%;
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/db_xref="taxon:9606"
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/clone_lib="Hr0243"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
                                                                                                                             AW379436 257 bp mRNA linear EST 04-FEB-2000 CM4-HT0243-081199-037-f03 HT0243 HOMO Sapiens CDNA, mRNA sequence.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM4&t2=CM4-HT0243-081199-037-f03&t3=1999-11-08&t4-1)
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
Query Match 29.4%; Score 301.4; DB Best Local Similarity 99.1%; Pred. No. 4e-61; Matches 324; Conservative 0; Mismatches
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High quality sequence stop: 357.
Location/Qualifiers
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DNA encoding human Human type IV coll Murine adipocytes-Porcine alpha2(I)

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1090 CAGGGCCCTCCTGGCTTCCAGGGCACTTCAGGCACCCTGGGGAGCCTGGGGGGCACCTTGGA
                                                                                    1150 CCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCAAGGCCCCCCC
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                                     CAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGA
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33..2262
34./2464 a /product "scavenger receptor-like protein"
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                                                                                                                                    The invention relates to a human scavenger receptor-like protein. The protein is useful as a target molecule for diagnosis, prevention and treatment of autoimmune diseases such as rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                         180
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                                                                                         new scavenger receptor-like protein for diagnosis, prevention and
treatment of autoimmune disease, such as rheumatoid arthritis -
                                                                                                                                                                                           100.0%; Score 1026; DB 24; Length 2262; 100.0%; Pred. No. 2.5e-251; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                          Sequence 2262 BP; 670 A; 576 C; 581 G; 435 T; 0 other;
                                                                                                                    Claim 3; Fig 1; 38pp; Japanese
                         27-MAR-2000; 2000JP-0090772.
                                                                                                                                                                                                              Conservative
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                                                             2002-144965/19
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Matches 1026; Conserv
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Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angloplasty;
low density lipoprotein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human scavenger receptor, designated SRCL-Pl. The SRCL-Pl polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic
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/product= "scavenger receptor"
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2000JP-0309068.
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P-PSDB; AAG63346.
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complications, bacterial infection and restenosis following angioplasty, which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products into
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                                        Sequence 2628 BP; 783 A; 661 C; 656 G; 528 T; 0 other;
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cancer;
disorder;
                               2334 CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACACTCATCT
CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCT
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2000WO-US30873
2000WO-US32678
2000WO-US34956
2001US-0767609
2001US-076609
2001US-076609
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2000US-220664P.
2000WO-US20710.
2000US-222695P.
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2000US-0665350.
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2001US-0802706.
2001US-0808689.
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2000WO-US23522.
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2000US-230978P.
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2000US-0709238.
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2001US-0854280.
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2001WO-US00000.
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28-FEB-2001;
01-MAR-2001;
09-MAR-2001;
14-MAR-2001;
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10-NOV-2000;
01-DEC-2000;
20-DEC-2000;
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22-JAN-2001;
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05-APR-2001;
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10-MAY-2001;
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Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO anteagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cardiac disorder; endothelial disorder; cardiac hypertrophy; atherosclerosis; hypertension; anglogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; arterial restenosis; anglia; rheumatoid arthritis; myocardial infarction; thrombophlebitis; lymphangitis; tumour anglogenesis; breast carcinoma; liver carcinoma;
                                                                                                                                                                                                                                                                                        CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCT 1020
                                                                                                                                                                                                                                                                                                                                                                                                       1378 GGCCAFGGGCCAGGAGAAGACTGTGCTTGATTTATGCTGGGCAGTGGAACGATTTC 1437
                                                                                                                                                                                                                                                                                                                                          1018 GGCCTCCTGGCCCATCAGGAGCGGTGGTGCCCTGGCCCTGCAGAATGAGCCAACCCCG
                                                                                                                                                     GCACCGGAGGACAATGGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTAT
                                                                                                                                                                                         TTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA
                                                                                                                                                                                                                                          CATCTTGTTTTCATAAACACTAGAGAGGAACAGCAATGGATAAAAAAACAGATGGTAGGG
                                                                                                                                                                                                                                                                                                                                                                                           GGCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTC
                                                                                       GGCCCTCCTGGCCCATCAGGAGCGGTGGTGCCCCTGGCCCTGCAGAATGAGCCAACCCCG
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2000US-219556P.
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20-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                537
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                                                                                                                                                                                                                 NF;
                                                                                                                                                                                                                                                                                        One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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Pred. No. 6.1e-251;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                       hypertrophy, trauma, cancer, age-related macular degeneration,
                                                                                                                                                                                        Gerritsen ME, Goddard, KJ, Marsters SA, Pan J, Marsters Ye W;
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                                                                                                                                                                                                                             Williams PM, Wood WI,
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L, Hillan KJ,
                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 27; 567pp; English
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Best Local Similarity 99.9%;
Matches 1025; Conservative
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Watanabe CK,
                                                            GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                       GERBER H.
GERRITSEN M E.
                                                                                                                       PAGNIN F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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BAKER K P.
FERRARA N.
                                                 GODDARD A.
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                                                                                                              PAN J.
PAONI
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ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
ABB8003. The PRO proteins and polynucleorides have cardiant, cytostatic,
antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic
activities, and can be used in gene therapy. The PRO polynucleotides,
proteins, agonists and antagonists are useful for treating or diagnosing
a cardiovascular, endothelial or angiogenic disorder in a mammal,
e.g. cardiac hypertrophy, trauma, cancer, age-related macular
degeneration, atherosclerosis, hypertension, arterial restenosis,
cegeneration, atheris, angina, myocardial infarctions, thrombophlebitis,
lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
carcinoma) and wound healing. The PRO polynucleotides have applications
in molecular biology, including use as hybridisation probes, and in
chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
probes used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal -
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L, Hillan KJ, Marsters SA, Pan J, Paoni
.K, Williams PM, Wood WI, Ye W;
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28-FEB-2001; 20010S-0796498.
28-FEB-2001; 20010S-0796498.
01-MAR-2001; 20010S-0806520.
09-MAR-2001; 20010S-08006689.
22-MAR-2001; 20010S-0806689.
22-MAR-2001; 20010S-0828366.
10-MAY-2001; 20010S-0854280.
10-MAY-2001; 20010S-0854280.
25-MAY-2001; 20010S-0856028.
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2000US-0747259
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25-JUL-2000;
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                                           GGCCCAACTGGCAACAAGGGACAGAAAGGAGAGAAGGGGGGAGCCTGGACCACCTGGCCCT
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ID AA160628 standard; cDNA; 2181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, can be a peripheral nervous injuries, peripheral nervous and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
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                                                                                  nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                            peripheral nervous system; neuropathy; central nervous system; CNS; Alzhbaimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                    Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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Yang Y,
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Xu C, Xue AJ,
Drmanac RT;
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                                                          Human polynucleotide SEQ ID NO 4617.
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Wang Z, Wehrman T, X
Zhou P, Goodrich R,
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Wang J, W
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                                                             Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J;
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Pred. No. 6.4e-251;
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Ku C, Xue AJ,
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                                     Human polynucleotide SEQ ID NO 1045
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Pang Z, Wehrman T, Xt
Zhou P, Goodrich R,
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2000US-0552317.
2000US-0598042.
2000US-0620312.
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2000US-0662191.
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2000US-0727344.
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            (first entry)
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Matches 1025; Conservative
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P-PSDB; AAM39686.
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09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                 The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-2, EXMAD-1, EXMAD-11, EXMAD-12, EXMAD-13, EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-17, EXMAD-17, EXMAD-17, EXMAD-17, EXMAD-18, EXMAD-18, EXMAD-21, EXMAD-23, EXMAD-24 and EXMAD-25. They are useful in the prevention and treatment of cancers, cell proliferation, cardiovascular, reproductive, immune, musculoskeletal, developmental and gastrointestinal disorders and inflammation.
                                                                                                                                                                                                                                                                                         Isolated polynucleotide encoding extracellular matrix or adhesion-associated protein (EXMAD) useful for diagnosing, treating, or preventing disorders associated with expression of EXMAD such as
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                                Extracellular matrix and adhesion-associated protein; EXMAD; cancer;
                                         inflammation; reproductive disorder; cardiovascular disorder; immune disorder; musculoskeletal disorder; developmental disorder; gastrointestinal disorder; cell proliferation disorder; ss.
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Pred. No. 6.8e-251;
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          coding
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           EXMAD-14
                                                                                                       WO200068380-A2
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                                                                                             CAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGA
                                                                                                                                                                                      CCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCAAGGGCCCCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human polynucleotide SEQ ID NO 69.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-OCT-2002 (first entry)
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1326 ATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATA 1385

1386 CTACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGAACGAAGGATCCCAGGGACCCCT

181

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241 GCGGGTGAGAGGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGCGGCGAAAGGA

TCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAG

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GGCCCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGGAAAGAGGGACTCCCCGGCCCT

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1686 CAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGA

CAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGA

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GCACCGGAGGACAATGGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTAT 1866 GCACCGGAGGACAATAGCTGCCCGCCTCGAAGAACTTCACAGAACAAATGCTACTAT

GCCCCTCCTGGCCCCATCAGGAGCGGTGGTGCCCCTGGCCCTGCAGAATGAGCCAACCCCG

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The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary deoxyribonucleic acid (CDNA) inserts (II), where the protein is substantially free from conternamealian proteins. (I) are useful for preventing, treating or ameliorating a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to angiogenesis, cytokine, cell proliferation, call differentiation, antinflammatory, stem cell growth factor activity and activin or inhibin-related activities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cils and peripheral nervous system disease, accidental damage or rese to neuroepithelial cells that can be used to sugment or replace contral and peripheral nervous system diseases and neuropathies, such as regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, amyotrophic activity, regulation of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia and for regeneration of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, platelet disorders such as thrombocytopaenia and for reagneration of haematopoiesis and is useful for treating myeloid or lymphoid cell disorders, various immune disorders including of periodontal disease. (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury or treating or stepororosis, osteoarthritis, bone degenerative disorders in creating avaious allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express tecombinant protein, as markers for tissues in which the corresponding protein is prate of a polyuncleoit the present of a polyuncleoit of the hyper ferentions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoImmune diseases, bone disorders and lung or liver fibrosis
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                                                                                                                                                                                                                                                                                                                                                                Evans
                                                                                                                                                                                                                                                                                                                                                            Collins-Racie LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 250; Page 231-232; 284pp; English.
                                                                                                                                                                                                                                                                                                                                                          LaVallie ER,
Spaulding V;
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99.9%;
                                                                              22-DEC-2000; 2000US-0745763
                                                                                                                          98US-0040963
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                                                                                                                                                                                       MCCOY J M.
LAVALLIE E R.
                                                                                                                                                                                                                                                                                            (TREA/) TREACY M. (SPAU/) SPAULDING V.
                                                                                                                                                                                                                                                                                                                                                            McCoy JM,
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                                                                                                                                                                                                                                                     EVANS C.
MERBERG D.
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                                                                                                                                                                      JACOBS K.
                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; ABP61859
US2002065394-A1.
                                                                                                                          18-MAR-1998;
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Merberg D,
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Matches 1025;
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(COLL/)
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(MERB/)
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                                                                                             GATGGGACATCTCCAGACTACAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGGTCAT
                                                                                                                                                  GGCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTC
                                                                                                                                                                AAV55746 standard; cDNA; 2930 BP.
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This DNA sequence was isolated from a human adult brain cDNA
library, and was designated clone bv227_1. The DNAs and proteins
are predicted to have biological activities which would make them
suitable for treating, preventing or ameliorating medical conditions in
humans and animals, although no supporting data is given. Suggested
activities include nutritional sources or supplements, immune
ctivities include nutritional sources or supplements, immune
ctissue growth activity, activity, hematopoiesis regulating activity,
chemotactic/chemokinetic activity, hemostatic and thrombolytic activity,
chemotactic/chemokinetic activity, and tumour inhibition activity. The DNAs
are also stated to be useful for gene therapy. A host cell transfected
with the DNA, or its subfragments and variants is useful for recombinant
                                                           Secreted protein; human; nutritional supplements; immune stimulant; immune suppressor; haematopoiesis regulator; tissue growth; chemotaxis; activin/inhibin; chemokinesis; haemostasis; thrombolysis; receptor/ligand activity; anti-inflammatory; tumour inhibitor; cadherin/tumour invasion suppressor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotides encoding secreted human proteins - derived from human foetal brain, adult brain, foetal kidney, adult ovary, adult retina, adult placenta or adult uterus cDNA libraries
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                                     Human secreted protein clone bv227_1 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  with the DNA, or its subfragments and variants i
production of the human secreted protein clones.
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Treacy M;
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9705-0868698
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           (first
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P-PSDB; AAW73628.
                                                                                                                                       Homo sapiens
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McCoy JM, R
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                                         CTACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCT
                                                                                  GGCCCAACTGGCAACAAGGGACAGAAAGGAGAGGAGGGGGAGCCTGGACCACCTGGCCCT
                                                                                                                           GCGGGTGAGAGAGGCCCAATTGGACCAGCTGGTCCCCCCGGAGAGGAGGGCGGCGAAAGGA
                                                                                                                                                                       TCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAG
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ATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATA
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RESULT 11 AAS71133

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Best Local Similarity 99.9 Matches 1025, Conservative

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Query Match

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Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angloplasty;
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  412 TCCAGTGGGGACCCCGGGCCCCCGGGCCACCAGGGAAAGAGGGGACTCCCCGGCCCTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleotide sequence of a human scavenger receptor.
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92..2320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The cand for chromosome confidentifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as (II). (II) is useful for generating antibodies against in medical imaging of sites expressing (II). (I) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in clasonable for genetic disorders or other traits to assess blodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64497-AAS94564 represent novel human cald aganostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed condition in the condition of the condi
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                                                                                                                                                                                             Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                               ONA encoding novel human diagnostic protein #6937
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Pred. No. 3.6e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 6937; 103pp; English.
AAS71133 standard; cDNA; 1521 BP
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99.8%;
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23-AUG-2000; 2000US-0649167
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                                                                                              (first entry)
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Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
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                                                                                                                                                                           TITICAGTIGAGAAAGAAATITITGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA 720
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                                                                                                                                                                                                                                                                                                                            GGCCCTCCTGGCCCATCAGGAGCGGTGGTGCCCTTGGCCCTGCAGAATGAGCCAACCCCG
                                                                                                                                                              GCCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTC
                                                               GCACCGGAGGACAATGGCTGCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of a human scavenger receptor.
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10-OCT-2000;
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                                                                                                                                                                                               New Scavenger receptor proteins SRCL-P1 with collectin-like structure, useful for treatment and diagnosis of diseases associated with oxidized
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                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2637 BP; 829 A; 617 C; 635 G; 556 T; 0 other;
                                                                                                                                                                                                                        low-density lipoprotein accumulation
                                                                                                                                                                                                                                              Claim 6; Page 88-93; 118pp; Japanese.
                                                                       2000JP-0035155
2000JP-0309068
                                             08-FEB-2001; 2001WO-JP00874
                                                                                                             PHARM IND LTD
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Matches 886; Conservative
                                                                                                                                                          WPI; 2001-497076/54.
P-PSDB; AAG63347.
WO200159107-A1
                                                                       14-FEB-2000;
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                        16-AUG-2001
                                                                                                                                     Wakamiya N;
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RESULT 15
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                                                 New Scavenger receptor proteins SRCL-P1 with collectin-like structure, useful for treatment and diagnosis of diseases associated with oxidized
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1870 AGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCTGCATTA 1927
                                                                                                                                                                                                                                                                                                                                                                                                lipoprotein and the binding of advanced glycation end-products into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCGGCTGCCCGCCTCACTGGAACTTCACAGACAAATGCTACTATTTTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      609 GGACAATGGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTATTTTCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 414.8; DB 22; Length 2256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2256 BP; 721 A; 524 C; 528 G; 483 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding novel human diagnostic protein #6935.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.3e-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 1.3e
0; Mismatches
                                                                                                                                                            Claim 4; Page 105-109; 118pp; Japanese.
                                                                                                        low-density lipoprotein accumulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 40.4%;
Best Local Similarity 87.0%;
Matches 468; Conservative
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P-PSDB; AAG63350
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess

Tang YT;

Liu C,

Drmanac RT,

(HYSE-) HYSEQ INC

WPI; 2001-639362/73

P-PSDB; ABG06944

30-MAR-2001; 2001WO-US08631

WO200175067-A2

11-0CT-2001

Homo sapiens.

2000US-0540217. 2000US-0649167.

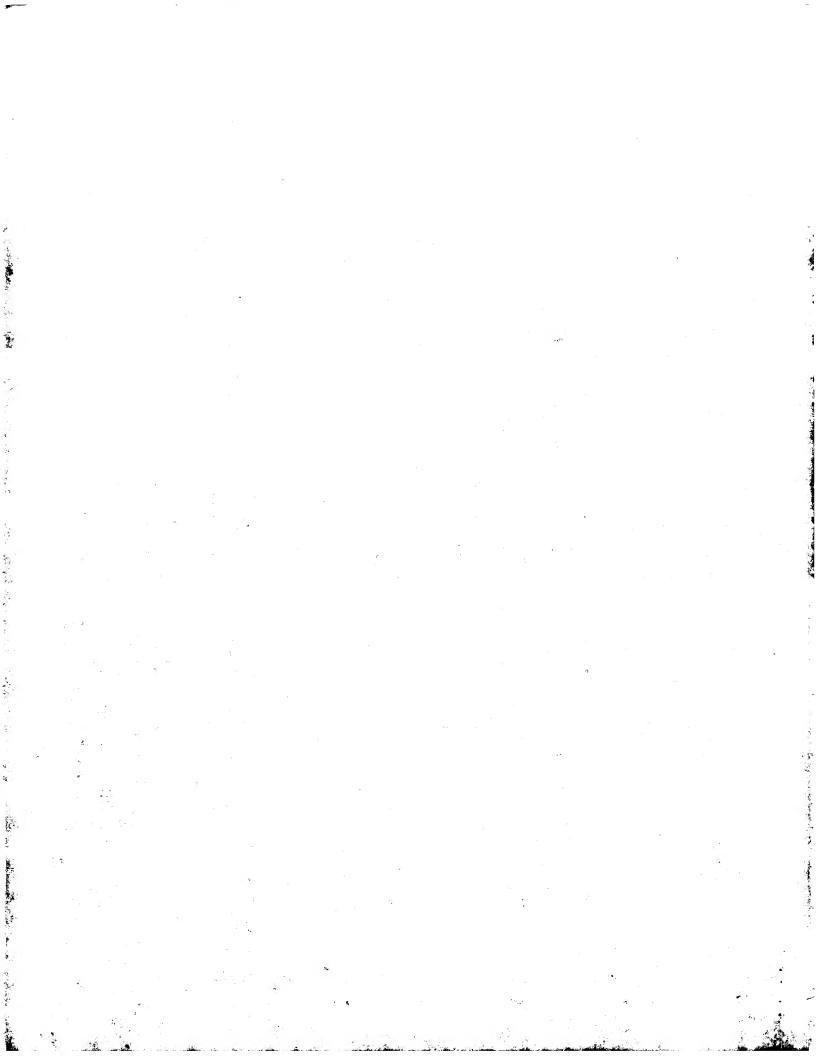
31-MAR-2000; 23-AUG-2000;

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags and entitying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and canno acid sequences. AAS64197-AAS94564 represent novel human DNA and diagnostic coding sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      870 GAAAGCTGGAC-AGCCGGATAACT-GGGGTCATGGCCCATGGGCCAGGAGAAGACTGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGTTGATTTATGCTGGGCAGTGGAACGATTTCCAATGTGAAGACGTCAATAACTTCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16.5%; Score 169.4; DB 23; Length 97.7%; Pred. No. 2.4e-33; cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 493 BP; 121 A; 116 C; 99 G; 157 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGCGAAAAAGACAGGAGACAGTACTGTCATCTGCATTA 1026
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 6935; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 214; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention. The CSR proteins are macrophage scavenger receptor proteins. The CSR proteins can be used in the treatment, gene therapy and disgnosis of diseases in which intracellular stress is important, such as arteriosclerosis, diabetic circulatory obstruction, and microbial infection. Expression of the proteins is induced in vivo in response to intracellular stress, and inhibits cell death as a result of such stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes the human cellular stress response 3 (CSR3) protein
                                                                                                               Cellular stress response protein; CSR1; CSR2; CSR3; human; macrophage; scavenger receptor protein; intracellular stress; arteriosclerosis; diabetic circulatory obstruction; microbial infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1406 TGCTCAGTGCCCGGCTGGACTCAACGTCCGGAACCTCTCCATGATCGTGGAGGAGTGA 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCCAATTGGACCAGCTGGTCCCCCGGAGAGAGGTGGCGGCAAAGGATCTAAAGGCTCCC 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 AGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATACTACAAGGTCCAC 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 CGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCTGGCCCAACTGGCA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 ACAAGGGACAGAAAGGAGAGAGAGGGGGAGCCTGGACCACCTGGCCCTGCGGGTGAGAGAG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 AGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGTGGGG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 TGATGAGGTCGAGGTTAGACACTGAAGTAGCCCAACTTATCAGTGATTATGGAAGAAATGA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 20; Length 3685;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              - for treatment and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 244; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3685 BP; 901 A; 1142 C; 972 G; 669 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.4%; Score 157.6; DB 2 55.5%; Pred. No. 5.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 142-150; 175pp; Japanese.
                                                                                    Human CSR3 protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                Scavenger receptor proteins – for disorders involving cell stress
AAX27858 standard; DNA; 3685 BP
                                                                                                                                                                                                                                                                98WO-JP03602
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                                                                                                                                                                                                                                                                                               98JP-0230121
                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-181032/15.
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                                                                                                                                                                                                                                                                                                           13-AUG-1997;
                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                               30-JUL-1998;
                                                         02-JUN-1999
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                                                                                                                                                                                                                                    25-FEB-1999
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

2983 bp mRNA linear PRI 21-NOV-2001 Homo sapiens CL-P1 mRNA for collectin placenta 1, complete cds. AB005145 AB005145.1 GI:17026100

RESULT 1
AB005145
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE

ORGANISM

REFERENCE AUTHORS

ALIGNMENTS

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Homo sapiens female tissue\_lib:placenta cDNA to mRNA.

Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Keshi,H., Sakai,Y., Fukuoh,A., Sakamoto,T., Itabe,H., Suzutani,T., Ogasawara,M., Yoshida,I. and Wakamiya,N.

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Result No.	t. Score	& Query Match	Length	DB	(I	Description
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(*)	12	80	4581		ECU62528	Equus
4.	119.	. 8	2010		Ö١	Human alpha
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GSRGSPĞKPGPQGPSGDPGPPGKEGLPGPQGPPGPQGLQGTVGEPGVPGPRGLPG
LEGYPGMPGPFKGPPGPSSAVVPLALQNEPTPAPEDNGCPFHWKNTDKCYYFSVB
KLEFEDAKLPCEDKSSHLVFTNTREEQQWIKKQMVGRESHWIGLTDSERENEWKUDG
TSPDXKNMKAQQPDNWGHGHPGBEDCAGLIYAĞQWNDFQCEDVNNFICEKDRETVLSS
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                                               C (bases 1 to 2983)
Ohtani, K.
Direct Submission
Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College,
Department of Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa,
Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:+81-166-68-2399)
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The membrane-type collectin CL-P1 is vascular endothelial cells J. Biol. Chem. 276 (47), 44222-44228 21570232
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/sex="female"
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1886 bp mRNA linear PRI 20-MAR-2002 DKFZp547G1215 (from clone DKFZp547G1215).

Homo sapiens mRNA; cDNA AL713657

HSM802985

LOCUS

ACCESSION VERSION

KEYWORDS

RESULT 2 HSM802985

GI:19584339

AL713657.1

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This clone (DKFZp547G1215) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@tzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="hypothetical protein"
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PEDNGCPPHWKNFTYRCXYYESPERGIFEDALLPGDKSSHLVFINTREDQWIKKQWY
GRESHWIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQW
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                                                                                                                                                                     clone from S. Wiemann, Molecular Genome Analysis, German Canc Research Center (DKFZ); Email s. Wiemann@dKz-heidelberg.de; Sequenced by BMFZ (Blomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGCAACAAGATTTGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATT
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                                                                         1 (bases 1 to 1886)
Coehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submission
Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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Pred, No. 3.2e-300;
0; Mismatches 1;
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/tissue_type="brain"
/clone_lbb="547 (synonym: hf
bh108; sites Not1 + SalI"
/dev_stage="fetal"
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/db_xref="taxon:9606"
/map="18p11.3"
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Patent: WO 0208284-A 27 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, US); Gerritsen, Mary E. (US); Goddard, Audrey (US); Goddwski, Paul J. (US); Gurney, Austin L. (US); Hillan, Kenneth J. (US); Marsters, Scot A. (US); Pan, James (US); Panni, Nicholas F. (US); Stephan, Jean-Philippe F. (US); Maranabe, Colin K. (US); Williams, P. Mickey (US); Wood, William I. (US)
                                                                                                                                                                                    Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A., Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J., Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I. and Ye, W.
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
493 c 491 q 415
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                                          1018 GGCCCTCCTGGCCCATCAGGAGCGGTGGTGCCCTGGCCCTGCAGAATGAGCCAACCCG
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Sequence 27 from Patent W00200690.
AX490920 GI:22323797
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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AX047353
Sequence 39 from Patent AX047353
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       Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoii,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
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                                           Compositions and methods for the diagnosis and treatment of disorders involving anglogenesis
Patent: WO 0200699-A 27 03-JAN-2002;
Genentech, Inc. (US)
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                                                                                                                                              Score 1337.4; DB 6
Pred. No. 3.3e-300;
0; Mismatches 1;
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                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
193 c 491 g 415
                                                                               Location/Qualifiers
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Best Local Similarity 99.9%;
Matches 1349; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2641)
Bandman,O., Hillman,J.L., Tang,Y.T., Lal,P., Yue,H., Baughn,M.R.,
Lu,D.A. and Azimzal,Y.
Extracellular matrix and adhesion-associated proteins
Patent: WO 0068380-A 39 16-NOV-2000;
Incyte Genomics, Inc. (US)
LocaliniOqualifiers
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/db_xref="taxon:9606"
/note="Incyte ID No: 4586187CB1"
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99.9%; Pred. No. 3.3e-300;
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       CCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCCC
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PRI 08-MAR-2001
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Nakamura, K., Funakoshi, H., Miyamoto, K., Tokunaga, F. and Nakamura, T.
Molecular cloning and functional characterization of a human
scavenger receptor with C-type lectin (SRCL), a novel member of a
                                                                                                                                                                                                                                                                                                                 AB038518 305B bp mRNA linear PRI 08-MAR-20
Homo sapiens SRCL mRNA for scavenger receptor with C-type lectin
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Nakamura, K. and Nakamura, T.

Nakamura, K. and Nakamura, T.

Direct Submission

Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medic:
School, Division of Biochemistry, Biomedical Research Center;
yamadaoka, Suita, Osaka 565-0871, Japan

(E-mail:knakamura@onbich.med.osaka-u.ac.jp,
Tel:81-6-6879-378310-7883), Fax:81-6-6879-3789)
2051 CCAATTACTGAAAAAAAATGACAGCTAGTGTTTTTTACCATCCGTCATTACCCAAAGAC
                                                                     2111 TIGGGAACTAAAATGTTCCCCAGGGTGATATGCTGATTTTCATTGTGACACATGGACTAA
                                                                                                                      1261 TCACATAGATTCTCCTCCGTCAGTAACCGTGCGATTATACAAATTATGTCTTCCAAAGTA
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                                                   TTGGGAACTAAAATGTTCCCCAGGGTGATATGCTGATTTTCATTGTGCACATGGACTGAA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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/db_xref="taxon:9606"
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/gene="SRCL"
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209. .2437
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SINSELESFRSDILDLRQQLOEITEKTSKNROPTLEKLOANGSDLVBQQQKRFTLQNN
SFLITTWRTLQAYNGYPNGYPNLQOPPSVLGARKDTDMLKEKVQSLQTLAANNSALA
KANNDTEEDMNSCLSSFTGQMDNITTISQANGSCKRDLQDLHKDTRRTAVRFSQLEE
RRQVFETDIVNIISNISYTAHHLRTLTSNLMDVRTTCTDTLFRHTDDLTSLNNTLVNI
RLDSISLENQQDMMRSKLDFVANLSYVMEEMKLVDSKHGQLIKNFTLLGQPPGPRGP
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Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T., Keshi,H.,
Sakai,Y., Fukuch,A., Sakamoto,T. and Wakamiya,N.
Direct Submission
Submitted (18-JAN-2002) Katsuki Ohtani, Asahikawa Medical College, Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa, Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:81-166-68-2333, Fax:81-166-68-2339)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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ILCALLTITVAILGYKVVEKMDNVSDGMETSHQTYDNKLTAVESDLKKLGDQAGKKAL
STNSELSTFRSDILDLRQQLQEITEKTSKNKDTLEKLQANGDSLVDRQSQLKETLQNN
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Molecular cloning of a mouse scavenger receptor with C-type lectin
(SRCI)(1), a novel member of the scavenger receptor family
Biochim. Biophys. Acta 1522 (1), 53-58 (2001)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mus musculus srcl mRNA for scavenger receptor with C-type lectin,
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GCATTATAACGGACTGTGATGGGATCACATGAGCAAATTTTCA---GCTCTCAAAGGCAAA
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RFQVFETDIVNISYTSAHHLRTITISNLDWWTTCTDTLTRHTDDLTSLNNTLVNI
RLDSISLRMQODMMRSKLDTEVANLSVYMEEMKLVDSKHGQLIKNFTILQGPPGFRGF
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Makamura, K. Funakoshi, H., Miyamoto, K., Tokunaga, F. and Nakamura, T. Makamura, K., Funakoshi, H., Miyamoto, K., Tokunaga, F. and Nakamura, T. Molecular cloning and functional characterization of a human scavenger receptor with C-type lectin (SRCL), a novel member of a blochem. Blophys. Res. Commun. 280 (4), 1028-1035 (2001)

E. Joses I to 4330)

Makamura, K. and Nakamura, T.

Direct Submission

Sobol of Medicine, Division of Blochemistry, Biomedical Research Center: 2-2 yamadaoka, suita, Osaka 55-0871, Japan

(E-mail:knakamur@onbich.med.osaka-u.ac.jp, Tel:81-6-6879-3783, Fax:81-6-6879-3783)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 3.2e-157;
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                       /gene="SRCL"
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Toppurished

Saldwin, J., Barna, M., Backerly, R., Baguslavkty, L., Boukhgalter, B.,

Baldwin, J., Barna, M., Backerly, R., Baguslavkty, L., Boukhgalter, B.,

Baldwin, J., Barna, M., Backerly, R., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Forreita, P., FitzHugh, W., Forrest, C., Funce, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

McDwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

McDwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Peterson, K., Pollara, V., Riley, R., Santos, R., Severy, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Nyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission

Nesearch, 320 Charles Street, Cambridge, MA 02141, USA

On Sep 9, 2000 this sequence version replaced gi:6649269.

All repeats were identified using Repeatmasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/Repeatmasker.html
                                                                                                                                               ACUIDLZ8 169088 bp DNA linear HTG 09-SEP-2000 Homo sapiens chromosome 18 clone RP11-324G2 map 18, WORKING DRAFT SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 169088)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone RP11-324G2
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Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 167512 bases at least Q40
Consensus quality: 16724% bases at least Q30
Consensus quality: 167996 bases at least Q20
Insert size: 177000; agarose-fp
Insert size: 168388; sum-of-contigs
Quality coverage: 6.2 in Q20 bases; sum-of-contigs
Quality coverage: 6.5 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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18044 22424: contig of 4381 bp in length
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4133 AGAAAAAGGTTATCAT 4148
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Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Homo sapiens genomic DNA Published Only in Database (1999)

2 (bases 1 to 188439)

2 (bases 1 to 188439)

Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission

Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical
                                                                                                                                                                                                                                                                              AP000915 188439 bp DNA linear PRI 27-APR-2002
Homo sapiens genomic DNA, chromosome 18p clone:RP11-720L2, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattoriéges.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
On Apr 26, 2002 this sequence version replaced gi:9188470.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                Db 153397 TCCTGGCCCATCAGGAGGGGTGCCCTGGCCCTGCAGAATGAGCCCAACCCCAGCACC 153338
  Db 153457 GGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCAAGGGCCCCCCGGGCC 153398
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                                            546 TCCTGGCCCATCAGGAGCGGTGGTGCCCTGGCCCTGCAGAATGAGCCAACCCCGGCACC
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99.6%; Pred. No. 9.3e-103;
iive 0; Mismatches 2;
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41134 c 40027 g 53275
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
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                                                                              49221 49320: gap of 100 bp 49221 66394: contig of 17074 bp in length 66395 66494: gap of 100 bp 66395 6494: gap of 100 bp 66395 91692: contig of 25198 bp in length 91693 91792: gap of 100 bp 120870 120869: contig of 29077 bp in length 120870 120969: gap of 100 bp 120870 120969: gap of 100 bp 120870 120969: gap of 48119 bp in length.
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22425 22524: gap of 100 bp
22525 38094: contig of 15570 bp in length
38095 38194: gap of 100 bp
38195 49220: contig of 11026 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
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llarity 99.6%; Pred. No. 9.2e-103;
Conservative 0; Mismatches 2;
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/note="assembly_fragment"
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91793. .120869
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18044 .22424
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/note="assembly_fragment
                                                                                                                                                                                                                                                                                                  /organism="Homo saplens"
/db_xref="taxon:9606"
/chromosome="18"
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arbitrary. Low-pass sequence sampling is useful for
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ACU24368 1108 71044 bp DNA linear HTG 28-FEB-2000 SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                             546 TCCTGGCCCATCAGGAGCGGTGGTGCCCTGGCCCTGCAGAATGAGCCAACCCCGGCACC 605
                                                                              for
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Submitted (28-FEB-2000) Whitehead Institute/MIT Center
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatWasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Manualia; Butheria; Primates; Catarrhini; Homir
1 (bases 1 to 71044)
12. Einten, Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RP11-179K3
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AUTHORS
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identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                        the record is updated, the accession number will be preserved.
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of 701 bp in length
100 bp
if 684 bp in length
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1596 1595; gap of 100 hn
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0845: gap of 100 bp 15325: contig of 690 bp in length 1635: gap of 100 bp 10 length 23232: contig of 694 bp in length 100 bp 1314: contig of 685 bp in length 3314: gap of 100 bp 100 bp 1318: gap of 684 bp in length 1898: contig of 684 bp in length
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34694; contig of 696 bp in length
3794; gap of 100 bp
3586; contig of 692 bp in length
3586; gap of 100 bp
36292; contig of 602 bp in length
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52062: contig of 708 bp in length
62: gap of 100 bp
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54409: contig of 663 bp in length
54509: gap of 100 bp
                    26874: gap of 100 bp
27563: contig of 689 bp in length
27663: gap of 100 bp
28355: contig of 692 bp in length
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26774: contig of 693 bp in length
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33114: contig of
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29145: conf
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187635 bp DNA linear HTG 30-MAY-2000
HOMO sapiens chromosome 18 clone RP11-815L4 map 18p11.3, WORKING
APOL1022
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                     Gaps
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Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Published only in DataBase (2000)
2 (bases 1 to 187635)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission
                                                                                                                                                                                                                                                                       GATCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTC
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 Length 71044;
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Center: RIKEN Genomic Sciences Center(GSC)
Center code: RIKEN
Web site: http://hgp.gsc.riken.go.jp/
Score 484.6; DB 2;
Pred. No. 8e-102;
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HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-815L4.
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35.8%;
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                 Best Local Similarity
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186345: contig of 1404 bp in length
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182895: contig of 1317 bp
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                                                                                                                                                                  Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 177020 bases at least Q40 Consensus quality: 177020 bases at least Q30 Consensus quality: 182105 bases at least Q20
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      Contact: hattori@gsc.riken.go.jp
                                               ------ Project Information
Center project name: HumDraft18
                                                                                                        Center clone name: RP11-815L4
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* NOTE: This is a 'working draft'
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Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Kitasato Univ., 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattoriegec.riken.go.jp, 778-9923, Fax:81-42-778-9924)

on May 31, 2000 this sequence version replaced gi:6997403.

Center: RIKEN Genomic Sciences Center(GSC)
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                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                      1 (bases) to 178022)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fuliyama, A., Yada, T., Totoda, Y., Watanabe, H. and Sakaki, Y. Fulished Only in DataBase (1999)
2 (bases 1 to 178022)
Hattori, M., Ishii, K., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fuliyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct, Submission
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Sequence updated (26-May-2000).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contags. The true order of the pieces
* is not known and their order in this sequence record is
                                                                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                       ORGANISM
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JOURNAL
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AUTHORS
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             KEYWORDS
                                                                                                                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.4%; Score 466.2; DB 2; Best Local Similarity 96.3%; Pred. No. 1.7e-97; Matches 488; Conservative 0; Mismatches 18;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 188255)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 123898 CTCCTGGCCCATCAGGAGCGGTGGTG-CCCTGGCCCTGCAGAATGAGCCAACCCCAGCAC 123956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Db 123658 AGGCTCCCAGGCCCCAAAGGCTCCCCGGGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCTC 123717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 123718 CAGTGGGGACCCAGGCCCCCGGGCCCACCAGGAAAGAGGGACTCCCCGGCCCTCAGGG 123777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 123838 GGGACTGCCAGGCTTGCCTGGGGTACCCAGGCATGCCAGGCCCCCAAGGGCCCCCCGGGC 123897
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 AGGTCCACCGGGCCCCCAGGGGTCCAAGAGTGACAGAGGATCCCAGGGACCCCTGGCCC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 TGAGAGAGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCTAA 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     366 CAGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGCCCTCAGGG
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                                                                                                                                                                                                                                                                                                                                                                                                1901 others
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| 34911 c 36303 g 50935 t
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HTG, HTGS_PHASE1; HTGS_DRAFT.
HOMO sapiens DNA, clone:RP11-839023.
HOMO sapiens
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DEFINITION
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AP000939/c
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                              24284 24383: gap of 100 bp 24384 46875: contig of 22492 bp in length 46876 65058: contig of 22492 bp in length 46976 65058: contig of 18083 bp in length 65059 65158: gap of 100 bp 65159 1322: contig of 16164 bp in length 81323 81422: gap of 100 bp 81422; gap of 100 bp 81424 98923: contig of 17401 bp in length 9824 110068: contig of 1145 bp in length 100 bp 81924 110068: contig of 1145 bp in length
                                                                                                                                                                                                                                                                                                                                                                                        122777 122816: gap of 100 bp 122817 122816: gap of 100 bp 133090 133189: contig of 10273 bp in length 133090 133189: contig of 10273 bp in length 133190 134126: contig of 8017 bp in length 141207, 141206: contig of 8017 bp in length 149307 149505: contig of 7744 bp in length 14951 149505: contig of 7744 bp in length 156106 156205: gap of 100 bp 156106 156205: gap of 100 bp 16206 162048: contig of 5843 bp in length 162149 165218: contig of 5843 bp in length 165119 165218: contig of 2262 bp in length 165219 165218: gap of 100 bp 165219 165218: gap of 100 bp 165219 165218 gap of 100 bp 165219 165280: gap of 100 bp 165219 165280: gap of 100 bp 165218 169386: contig of 2406 bp in length 165987 170086: gap of 100 bp 170087 171999: contig of 1823 bp in length 170087 171999: contig of 1823 bp in length 170107 172009: contig of 1823 bp in length 170107 172009: contig of 1823 bp in length
                                                                                                                                                                                                                                                                                                                                      110069 110168: gap of 100 bp 122716: contig of 12548 bp in length 122717 122816: gap of 100 bp 100 bp
                                                                               24283: contig of 24283 bp in length
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176372 178022: contig of 1651 bp in length.
Location/Qualifiers
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* arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved.
                                 NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163175 163241: gap of 100 bp 163275 167066: contig of 3792 bp in length 167067 170120: contig of 3792 bp in length 167067 170120: contig of 2954 bp in length 170121 170220: gap of 100 bp 170221 172530: gap of 100 bp 172531 175599: contig of 2210 bp in length 172531 175599: contig of 200 bp 175599 17718: contig of 100 bp 175699 17718: contig of 100 bp 17719 177219: contig of 1313 bp in length 178532 178631: gap of 100 bp 178531: contig of 1313 bp in length 178532 178631: gap of 100 bp 178531: contig of 1313 bp in length 178532 178653: contig of 1206 bp 178632 178633: contig of 1206 bp 178633 178633: contig of 1206 bp 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 178633 17
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16197 33789: contig of 17593 bp in length
33790 33889: gap of 100 bp
33890 51010: contig of 17121 bp in length
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181165 187735; contig of 1571 bp in length

182736 182835; gap of 100 bp

182836 183923; contig of 1088 bp in length

183394 184023; gap of 100 bp

184024 185810; contig of 1787 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75156: gap of 100 bp
84737: contig of 9581 bp in length
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90909: contig of 6072 bp in length
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                                                                                                Published Only in DataBase (1999)

2 (bases 1 to 18825)

Rattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Rujyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

Submitted (I7-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (REN), Genomic Sciences Center (GSC):

Kitasato Univ., 1-15-1 (KIERN), Genomic Sciences Center (GSC):

Kitasato Chiv., 1-15-1 (KIERN), Tel:81-42-778-9923,

Pax:81-42-778-9924)

On May 31, 2000 this sequence version replaced gi:6997751.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         soon as it is available and the accession number will be
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens 188,255 genomic DNa of 18p11.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
------- Project Information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246 TGAGAGAGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGGCGTGGCGGCAAAGGATCTAA 305
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Matches 438; Conservative 0;
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116, App 94, Appl 137, App 10, Appl 63, Appl 98, Appl

372, App 647, App 726, App 624, App 693, App 1, Appl1

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120 ACTACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCC 179
 Sequence Seq
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 9.0%; Score 121.6; DB 1; Length Best Local Similarity 53.9%; Pred. No. 3.7e-22; Matches 250; Conservative 0; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 94111-4187
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
           US-09-453-702B-66
US-09-404-819A-372
US-09-134-001C-726
US-09-134-001C-624
US-09-134-001C-624
US-09-134-001C-624
US-09-134-001C-634
US-09-453-702B-116
US-09-453-702B-137
US-09-453-702B-137
US-09-453-702B-137
US-09-453-702B-137
US-08-147-509B-98
US-08-147-509B-98
US-08-377-509B-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
TELEPHONE: (415) 494-8771
TELEFAX: (415) 494-8771
INFORMATION FOR SEQ ID NO: 60:
                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
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LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
CLASSIFICATION: 435
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TOPOLOGY: line

MOLECULE TYPE: C

DESCRIPTION: /
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US-08-642-255-60
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8700.356 Million cell updates/sec
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                                                                                                           March 21, 2003, 02:00:05; Search time 47.7621 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-08-155-888-1
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S-09-249-200-5
S-08-794-795-1
S-09-249-200-1
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US-08-893-467A-1
US-08-555-669-11
US-09-073-663-11
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               GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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102 ACCACCGGGTGCACCTGGCCCAGCGGGTCCGCCTGGATCTAGAGGTGACCCAGGACCGCC 161
                                                                         162 TGGTGCTCCGGGACCTGCAGGCCCACCGGGTAGCCGTGGCGATCCGGGACCACCGGGTGC 221
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                                     240 TGCGGGTGAGAGAGGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAGCGTGGCGGCAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 TGGCGATCCGGGACCACCGGGTGCACCTGGCCCAGCGGGTCGGC 565
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND. Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 50, Application US/08642255 Patent No. 5773249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-871
TELES: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
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LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                           Gaps
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  Length 756
Score 118; DB 1; Length 75 Pred. No. 3.1e-21; 0; Mismatches 200; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: DILWORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/655,086 FILING DATE: 03-JUN-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 2044.0.;
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOTT A.
APPLICANT: BUECHTER, DOUGLAS
APPLICANT: ZHANG, GUANGHUI
APPLICANT: CONNOLLY, KEVIN
APPLICANT: CONNOLLY, KEVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08655086
Patent No. 5821089
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NAME: STEEN, DEFERSY S.
REGISTRATION NUMBER: 203-
REFERENCE/DOCKET NUMBER: 203-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-228-8484
TELEPHONE: 516-228-8516
Query Match 8.7%;
Best Local Similarity 54.3%;
Matches 238; Conservative
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CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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COUNTRY:
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A55556-3/BIR
                                                                                                                                                                                          MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic'
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 20,015
                REFERENCE/DOCKET NUMBER: ASTELECOMMUNICATION INFORMATION
                                          TELEPHONE: (415) 494-8700
TELERAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO. 48:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                       Query Match 7.8%;
Best Local Similarity 54.0%;
Matches 217; Conservative
                                                                                                                           LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: OTHER INFORMATION:
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LENGTH: 1608
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                                                                                                                                                            Indels
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APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
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4 Embarcadero Center, Suite 3400
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                                                                                                                                                           0; Mismatches 224;
                                                                                                                             DB 1;
                                                                                                                           Score 113.6; DB 1
Pred. No. 7.6e-20;
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Patent No. 5773249
GENERAL INFORMATION:
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                                                                                                                             Query Match
8.4%;
Best Local Similarity 52.5%;
Matches 248; Conservative
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             LENGTH: 3181 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS
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STATE: California
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CLASSIFICATION: 435
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                                                           TOPOLOGY: unknown ; MOLECULE TYPE: CDNA US-08-655-086-1
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STREET: 4
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      Length 432
Score 106; DB 1; Length 43
Pred. No. 3e-18;
0; Mismatches 185; Indels
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Pred. No. 5.2e-18;
0; Mismatches 205; Indels
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APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER TILLE OF INVENTION: NOVEL PROCOLLAGENS
FILLE REPERBENCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENTIN VET. 2.0
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Best Local Similarity 52.8
Matches, 229; Conservative
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                                                                                                                                       247 GAGAGAGCCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCTAAA 306
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 GGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCTGGCCCA
                                                                                                     421 GCTGGCAAACATGGAAACCGTGGTGAAACTGGTCCTTCTGGTCCTGTTGGTCCTGCTGGT
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                                                                   187 ACTGGCAACAAGGACAGAAAGGAGAGAGGGGGAGCCTGGACCACCTGGCCCTGCGGGT
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APPLICANT: Reeders, Stephen T.
APPLICANT: Zhou, Jing
TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method
TITLE OF INVENTION: of Detecting Collagen Deficiency
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,465
FILING DATE: 27-AUG-1993
ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5731192
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REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 403
TELECOMMUNICATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 5102 base pairs
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20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 GGGTGAGAGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATC
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STREET: 246 Church Street
CITY: New Haven
                                                                                                          join(2..82, 86..97, 101..4399, 4403..4420, 4424
..4465, 4469..4876, 4880..5101)
                                                                                                                                                                                               Length 5102;
                                                                                                                                                                                               Score 100; DB 1; Length 51
Pred. No. 3e-16;
0; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alpha-3 Chain Type IV Collagen
Polynucleotides
23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 800K storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/07/621,091G
FILING DATE: 11/30/90
CLASSIFICATION: 424
PRIOR APPLICATION DATA: NO. 5424408 applicable
ATORNEY/AGENT INFORMATION:
NAME: Barth, Richard S.
RECISTRATION NUMBER: 28180
REFERENCE/DOCKET NUMBER: 900983/RB
                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh OS7.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/07621091G
Patent No. 5424408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Microsoft Word 5.1a CURRENT APPLICATION DATA:
                                                                                                                                                                                                 h 7.4%;
Similarity 52.4%;
                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
TYPE: nucleic acid
STRANDEDNESS: doub:
TOPOLOGY: linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Connecticut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                       CCATION:
COCATION:
US-08-494-168-1
                                                                                       NAME/KEY:
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US-07-621-091G-1
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STATE: Co
                                                                                                                                                                                                                                             220;
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Best Local S
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FILE REFERENCE: 951263A
CURRENT APPLICATION NUMBER: US/08/399
CURRENT FILING DATE: 1995-03-07
EARLIER APPLICATION NUMBER: 07/621091
EARLIER FILING DATE: 1990-11-30
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                   ) NAME/KEY: CDS
; LOCATION: (1)..(1416)
US-08-399-889-1
                                                                                                                                                                   ORGANISM: Calf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Calf
                                                                                                                                      LENGTH: 1416
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LENGTH: 1416
                                                                                                                                                       TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T
APPLICANT: Morrison, Karen E
APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.4%; Score 99.6; DB 1; Length 1
51.6%; Pred. No. 2.2e-16;
tive 0; Mismatches 214; Indels
                                                                                                                                                                                                                                                                                                                                                                POSITION IN GENOME: No. 5424408 known CHROMOSOME/SEGMENT: No. 5424408 known PUBLICATION INFORMATION: No. 5424408e
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
TELEX: 236268
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1416 base pairs
TYPE: NUCLEIC acid
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                                                                                                                                         JOPOLOGY: Linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                               LIBRARY: Bovine lens cDNA CLONE: KMC15
                                                                                                                                                                                                                                                                                                 CELL TYPE: Whole kidney IMMEDIATE SOURCE:
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POSITION IN GENOME:
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US-08-399-889-1
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127 GGTCCACCGGGCCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCA 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 AGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGGCCCTCAGGGC 426
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Sequence 1, Application US/09167364

Patent No. 6007980

GENERAL INOFMATION:
GENERAL INOFMATION:
APPLICANT: Reeders, Stephen T

APPLICANT: Hudson, Karen E

APPLICANT: Hudson, Bally G

TILLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides

CURRENT APPLICATION NUMBER: US/09/167,364

CURRENT FILING DATE: 1998-10-07

EARLIER PFLICATION NUMBER: 08/399889

SARLIER FILING DATE: 1995-03-07

NUMBER OF SEQ ID NOS: 25

CORPUSABLE APPLICATION NUMBER: 08/399889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.4%; Score 99.6; DB 2; Length 1 Best Local Similarity 51.6%; Pred. No. 2.2e-16; Matches 228; Conservative 0; Mismatches 214; Indels
US/08/399,889B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547 CCTGGCCCATCAGGAGCGGTGG 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      703 ACTGGACCACCTGCAGCAGGG 724
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343 CCAGGCATGAAAGGGAAGAAGGGTAATTCAGGATTTCCAGGACCACGACCTCCAGGG 402
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ADDRESSEE: Minnich & McKee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 44114-2518
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 720 Kb storable
COMPUTER: IBM PS/2, Model 35 SX
OPERATING SYSTEM: DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/08/392,367B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08392367B Patent No. 5691197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1868 base pairs
TYPE: Nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24,175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Minnich, Richard J. REGISCRATION NUMBER: 24.175
REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/3
                                                                                                                                                                                                                                                                                                                                                                           CCTGGCCCATCAGGAGCGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Minnich, Richard J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Cleveland STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                     127 GGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCA 186
                                                                                                                                                                                                                                                                                       GAGAGAGGCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGCAAAGGATCTAAA 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 GGTCCACCGGGCCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCTGGCCCA 186
                                                                                                                     Gaps
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Patent No. 6277558
CEBREAL INFORMATION:
APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 95-1263-C
CURRENT PAPLICATION NUMBER: US/09/439,897
UNMBER OF SEQ ID NOS: 65
                                                                                  Length 1416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1416;
                                                                                Score 99.6; DB 3; Length 1.
Pred. No. 2.2e-16;
0; Mismatches 214; Indels
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Pred. No. 2.2e-16;
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                                                                                  7.4%;
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                                                                                                    Best Local Similarity 51.6
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1416)
US-09-167-364-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)..(1416)
US-09-439-897-1
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ORGANISM: Bos taurus
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Matches 228; Conserv
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US-09-439-897-1
                                                                                  Query Match
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APPLICANT: Elomaa, Outi
APPLICANT: Elomaa, Outi
APPLICANT: Kangas, Maarit
APPLICANT: Kangas, Maarit
TITLE OF INVENTION: An Insolated DNA Sequence For a
Patent No. 5691197
TITLE OF INVENTION: No. 5691197el Macrophage Receptor with
TITLE OF INVENTION: a Collagenous Domain and the
TITLE OF INVENTION: Polypeptide Chain Encoded by
TITLE OF INVENTION: Such a Sequence
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TOPOLOGY:
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                                                                                                                                            124 CAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCCAGGGACCCCCTGGC 183
                                                                                                                     Gaps
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                                                                                        / Match 7.3%; Score 99.4; DB 1; Length 1868; Local Similarity 51.5%; Pred. No. 2.8e-16; les 229; Conservative 0; Mismatches 216; Indels 0
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TOPOLOGY: Linear
MOLECULE TYPE: Nucleotide-genomic DNA
HYPOTHETICAL: No. 5691197 relevant
ANTI-SENSE: No. 5691197 relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
MEDIUM TYPE: 720 Kb storable
TYPE: 720 Kb storable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 CCTCCTGGCCCATCAGGAGCGGTGG 568
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STREET: Suite 700
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OPERATING SYSTEM:
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44114-2518
                                                     ; ANTI-SENSE:
US-08-392-367B-1
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CCCATGGGGTCCCCTGGAGCTCAGGGAGGTAAAGGTGATGCTGGAAAACCAGGCCTACCA 1020
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APPLICANT: Brewton, Richard G.
APPLICANT: Mayne, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 7.3%; Score 99.4; UB 3; Best Local Similarity 51.5%; Pred. No. 2.8e-16;
                                                                                                          NAME: Minnich, Richard J.
REGISTRATION NUMBER: 24,175
RERENCE/DOCKET NUMBER: TRV 2 009
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 861-5582
TELEFAX: (216) 241-1666
TELEFAX: (216) 980162
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1868 base pairs
TYPE: NUCLeic acid
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STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: Nucleotide-genomic DNA HYPOTHETICAL: No. 6063901 relevant ANTI-SENSE: No. 6063901 relevant
                      US/08/893,467A
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Patent No. 5773248
                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    Single
CURRENT APPLICATION DA APPLICATION NUMBER:
                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                          Linear
                                                                                                                                                                                                                                                                                                                                                              TYPE: Nucleic
STRANDEDNESS:
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ANTI-SENSE: N
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CITY: Houston
STATE: Texas
COUNTRY: USA
                                                                                                                                          Houston
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LOCATION:
                                                                                                  ADDRESSEE:
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                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/555,669
FILING DATE: 13.NOV-1995
                                                                                                                                                                                                                                                                               8389-030
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                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-073-663-11
; Sequence 11, Application US/09073663
                                                                                                                                                                                                           CLEASTILLATION: 433
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8389-
TELECOMMUNICATION INFORMATION:
TELEFAX: 415-854-360
TELEFAX: 415-854-369
TELEFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 51.5%
Matches 229; Conservative
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47..2098
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                                                                                                                                                                                                   CLASSIFICATION:
USA
                  10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY:
LOCATION:
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COUNTRY:
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124 CAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGC 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 GGTGAGAGAGGCCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCAAAGGATCT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AAAGGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGC 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    824 GCGCCTGGGAAAGCGGGTGACCGAGGCGAAGGGCCCCAGAAGGGTTCCGCGGCCCCAAG 883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGTGACCTCGGCAGACCTGGTCCCAAGGGAACCCCCGGAGTGGCCGGGCCAAGCGGAGAG 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCCCGGC 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       764 CTCGGGCCCCCTGGGGACCGGGGTCCCATTGGGTTCCGAGGGCCGCCTGGGATCCCAGGA 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 CCCAGTGGGGACCCCAGGCCCCCCGGGCCCACAGGCAAAGAGGGACTCCCCGGCCCTCAG 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2543;
Patent No. 6127523
GENERAL INFORMATION:
APPLICANT: Brewton, Richard G.
APPLICANT: Mayne, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 7.3%; Score 99.4; DB 3; Length 2 Best Local Similarity 51.5%; Pred. No. 3.2e-16; Matches 229; Conservative 0; Mismatches 216; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFCATION:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERRENCE/DOCKET NUMBER: D5913D
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS 8.1
SOFTWARE: Microsoft WORD for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,663
                                                                                                                                                                                                     E: McGregor & Adler, LLP
8011 Candle Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
47..2098
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STRANDEDNESS: unkno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  227 GACCACCTGG-----CCCTGCGGGTGAGAGGCCCCAATTGGACCAGCTGGTCCCCCCG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 ---AGGGACCCCCTGGCCCAACTGGCAACAAGGGACAGGAAAGGAGAAAGGGGGGAGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.2%; Score 97.6; DB 4; Length 4359; Best Local Similarity 52.3%; Pred. No. 1.2e-15; Matches 272; Conservative 0; Mismatches 234; Indels 14
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ORGANISM: Homo sapiens

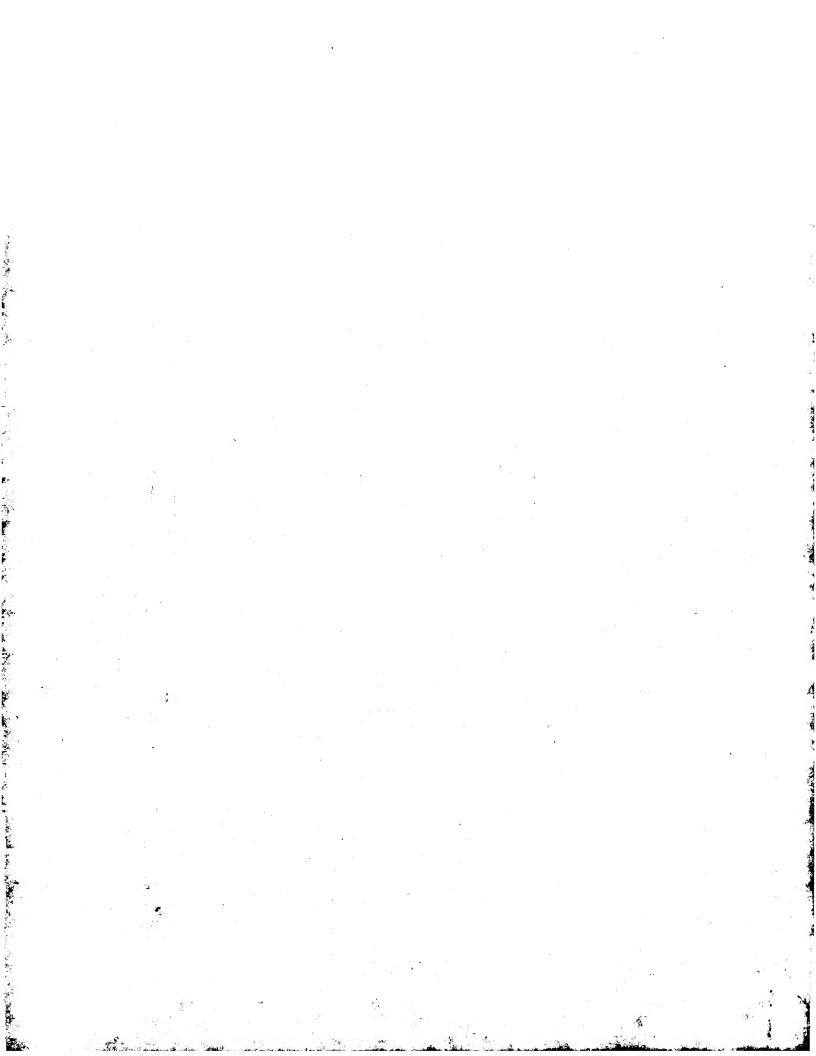
FEATURE:

NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No. 6426186 331365 (1553795CB1)

US-09-484-970B-4
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                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JONES, Karen A.
APPLICANT: Walker, Michael G.
APLICANT: Walker, Michael G.
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
SOFTWARE: PERL PROGRAM
                    1004 GAGGCTGGTCGCAACGGTGCTCCGG 1028
544 CCTCCTGGCCCATCAGGAGCGGTGG 568
                                                                                                              Sequence 4, Application US/09484970B Patent No. 6426186
                                                                             RESULT 15
US-09-484-970B-4
                                                                                                                                                                                                                                                                                                                                 LENGTH: 4359
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Search completed: March 21, 2003, 08:26:12 Job time : 66.7621 secs



App App App App

Sequence 104 Sequence 725 Sequence 448 Sequence

448,

sequence 98, Appl Sequence 3685, Appl Sequence 246, Appl Sequence 613, Appl Sequence 613, Appl Sequence 613, Appl Sequence 331, Appl

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Merberg, David
Treacy, Maurice
Spaulding, Vikk
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                       0 US-10-001-835-98

0 US-09-880-107-3685

0 US-09-978-295A-613

US-09-978-295A-613

US-09-978-192A-613

US-09-99-812A-613

US-09-99-812A-613

US-09-99-812A-613

US-10-174-590-331

US-10-175-758-331

US-10-175-738-331

US-10-175-738-331

US-10-175-738-331

US-10-175-738-331

US-10-175-738-331

US-10-176-757-331

US-10-180-552-331

US-10-180-552-331

US-10-180-552-331

US-10-180-552-331

US-10-180-552-331

US-10-180-552-331
                                           US-10-044-090-448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CILL. TAR
STATE: MA
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sprunger, Suzanne A.
REGISTRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
INFORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCoy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 198, Application US/09745763
Patent No. US20020065394A1
GENERAL TARORMATION:
APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 2930 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
Evans, Chery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                             US-09-745-763-198
                                           Sequence 198, App Sequence 1975, App Sequence 782, App Sequence 57, App1 Sequence 64, App1 Sequence 64, App1 Sequence 206, App Sequence 206, App Sequence 22, App1 Sequence 22, App Sequence 25, App Sequence 26, App Sequence 26, App Sequence 26, App Sequence 26, App Sequence 786, App Sequence 6, App1 Sequence 6, App1 Sequence 786, App Sequence 6, App1 Sequence 762, App Sequen
                                                                                                   March 21, 2003, 01:57:56 ; Search time 206.471 Seconds
   (without alignments)
   5089.177 Million cell updates/sec
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1 atgcaacaagatttgatgag......agaaaaaggttatcatcccg 1355
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published_Applications_NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/Dec_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
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             GenCore version 5.1.4\_p5\_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-954-456-11975

US-09-984-456-11975

US-09-980-107-3346

US-09-924-340-57

US-09-925-302-64

US-09-925-301-42

US-09-925-301-42

US-09-925-299-206

US-09-925-299-206

US-09-925-299-206

US-09-925-299-206

US-09-925-299-206

US-09-925-299-206

US-09-925-299-206

US-10-041-887-33
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US-09-954-456-786
US-09-980-U07-2094
US-09-919-497-6
US-09-954-456-762
                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
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                                                                                                                                                                  US-09-763-712A-1_COPY_670_2024
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                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                         nucleic search, using sw model
                                                                                                                                                                                                                                IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                           length: 0
length: 200000000
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110
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Match
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110.6
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109.4
107.2
                                                                                                                                                                    Title:
Perfect score:
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249
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106
105.4
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Maximum DB
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ALIGNMENTS

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APPLICANI: TOURY, PAUL
TITLE OF INVENTION: Dets
FILE REFERENCE: 68920-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT APPLICATION NUMBER: US/09/23,617
PRIOR PAPLICATION NUMBER: US/60/23,617
PRIOR PLING DATE: 2000-09-18
PRIOR FLING DATE: 2000-09-25
PRIOR FLING DATE: 2000-09-25
PRIOR FLING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR PRILICATION NUMBER: US/60/235,720
PRIOR PRILING DATE: 2000-09-27
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                                                                                                                                                                               CCAATTACTGAAAAAAATTGACAGCTAGTGTTTTTTACCATCCGTCATTACCCAAAGAC
                                                                                                                                        Length
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                                                                                                                                                                                                                                                                                                                                                 TGGAACACTCCAATCAGAAAAAGGTTATCAT 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 249;
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/60/235,863 PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/09954456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEY: misc_feature
INFORMATION: n=a,t,g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version
SEQ ID NO 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1975, Application
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-954-456-1975/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                     1021
                                                                                               2286
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                                                                                   Length 2930
                                                                                                              Indels
                                                                                  DB 10;
                                                                                                             2;
                                                                                Score 1335.8;
Pred. No. 0;
                                                                                                             0; Mismatches
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 198:
                                                                                98.68;
                                                                                                            Matches 1348; Conservative
                                                                                                Similarity
                                                      US-09-745-763-198
                                                                                  Query Match
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                                                                 CGGGTGAGAGAGCCCCAATTGGACCAGCTGGTCCCCCGGAGAGCGTGGCGGCGAAAGGAT
                                                                                                                                                                                           302 CTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: NOCKLEY, JOSEPH G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Experssion Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN VET. 2.1
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US-09-880-107-3946
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8.2%; Score 111; DB 10;
Best Local Similarity 53.0%; Pred. No. 9.1e-19;
Matches 237; Conservative 0; Mismatches 210;
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Patent No. US20020142981A1
GEMERAL INFORMATION:
APPLICANT: Horne, Darci T.
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ORGANISM: Homo sapiens
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LENGTH: 6728
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GENERAL INFORMATION:

TITLE OF INVENTION: Sets

CURRENT FILING DATE: 2001-09-18

FRIOR PRILOGATION NUMBER: US/60/234,052

PRIOR FILING DATE: 2000-09-18

PRIOR APPLICATION NUMBER: US/60/234,052

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

PRIOR FILING DATE: 2000-09-27

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                                                                                            CCAAAGACTTGGGAACTAAAATGTTCCCCAGGGTGATATGCTGATTTTCATTGTGCACAT 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             236 GGACTGAATCACATAGATTCTCCTCCGGTGAGGTAACGGATTATACAAATTATGCTT 177
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                                                                                                                                122 TACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTG 181
                                    Gaps
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9.1e-19;
   No. 1.3e-55;
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53.0%; Pred. No. 9
   Pred.
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Patent No. US20020115057A1
GENERAL INFORMATION:
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SEQ ID NO 782
LENGTH: 6728
95.3%;
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NUMBER OF SEQ ID NOS: 2276
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                             266; Conservative
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ORGANISM: Homo sapiens
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.054.DIV
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52.9%; Pred. No. 4.4e-19;
iive 0; Mismatches 229;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/992,600A CURRENT PELLING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR PELING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR PILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/296,698
PRIOR APPLICATION NUMBER: US 60/295,574
PRIOR APPLICATION NUMBER: US 60/293,574
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57, Application US/09992600A Publication No. US20030027161A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        561 AGCGGTGGTGCCCTGCCTGCAG 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  589 TGAACCTGGTGCCATGGGACCCCAG 613
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Matches 267; Conservative
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1118..1133
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US-09-992-600A-57
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TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.022.REG
CURRENT APPLICATION WUMBER: US/09/924,340
CURRENT APPLICATION NUMBER: US 60/305,456
FRIOR PAPLICATION NUMBER: US 60/305,456
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-29
FRIOR FILING DATE: 2001-06-15
FRIOR APPLICATION NUMBER: US 60/293,574
FRIOR FILING DATE: 2001-06-15
FRIOR FILING DATE: 2001-06-15
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                                                                                                                                                                                                                                                                                    542 GCCCTCCTGGCCCATCAGGAGCGGTGG 568
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Publication No. US20030027248A1
GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
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LENGTH: 1133
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US-09-924-340-57
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NAME/KEY:
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   124 CAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGC 183
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                                                                                                                                                                  CCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCCC
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Patent No. US20020052308A1
GENERAL INPORMATON:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT RAPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR RELING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 2192
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                      169 CAGAGGAGGGAGCCCCAAGGTAACTCCGGTGAGAAGGGCGACCAGGGATTTCAAGG 228
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| Sequence 64, Application US/09925302
| Patent No. US20020044941A1
| GENERAL INFORMATION:
| APPLICANT: Rosen et al.
| TILLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA104
| CURRENT APPLICATION NUMBER: US/09/925,302
| CURRENT PILING DATE: 2001-09-10
| PRIOR APPLICATION NUMBER: PCT/US0/05918
| PRIOR APPLICATION NUMBER: 60/124,270
| PRIOR PPLICATION NUMBER: 60/124,270
| PRIOR FILING DATE: 1999-03-12
| NUMBER OF SEQ ID NOS: 896
| SEQ ID NO 64
| CURRENT PILING DATE: PA104
| PRIOR FILING DATE: PA104
| PRIOR FILING DATE: 2090-03-12
| NUMBER OF SEQ ID NOS: 896
| SEQ ID NO 64
| CURRENT PILING DATE: PA104
| CURRENT PILING DATE: PA104
| CURRENT PILING DATE: PA104
| CURRENT PILING DATE: L999-03-12
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LOCATION: (2653)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (2667)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (2687)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (2683)
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APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SOD ID NOS: 3950
SOFTWARE: PatentIn Ver: 2.1
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tive 0; Mismatches 235; Indels
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Patent No. US20020142981A1
GENERAL INFORMATION:
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Best Local Similarity 51.3
Matches 248; Conservative
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LOCATION: (1)..(5086)
OTHER INFORMATION: n =
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US-09-880-107-3947
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Fublication No. US20030040617A9
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR PPLICATION NUMBER: PCT/US00/05883
PRIOR PPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
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LOCATION: (4)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
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LOCATION: ($126)
OTHER INFORMATION: n equals a,t,g, or NAME/KEY: misc_feature
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; OTHER INFORMATION: n equals a,t,g, or
US-09-925-299-206
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Best Local Similarity
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                                                                                1012 CTCCGGCCCCGTTGGACCTCCTGGTAATCCTGGAGCAAACGGCCTTACTGGTGCCAAGGG 1071
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                                                             360 GGGCCCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGCAAAGAGGGACTCCCCGGCCC 419
                                                                                                                                                                                                                                                         540 CGGCCCTCCTGGCCCATCAGGAGCGGTGGTGCCCCTGGCCCTGCAGAATGAGCCAACCCC 599
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300 ATCTAAAGGCTCCCAGGGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCA 359
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                                                                                                                                                                                         480 ACCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCCATGCCAGGCCCCCAAGGGCCCCC
                              892 GICTGCTGCCCTCCAGGCTTCCCAGGTGCCCCTGGCCCCAAGGGTGAAATTGGARCTGT
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIO.
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR FILING DATE: 2001-08-10
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PATENTIN VET. 2.0
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 206
LENGTH: 5145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%; Score 107; DB 10; Length 5 Best Local Similarity 51.3%; Pred. No. 8.8e-18; Matches 248; Conservative 0; Mismatches 235; Indels
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: LOCATTON: (5143)

: OTHER INFORMATION: n equals a,t,g, or c

US-09-925-299-206
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LOCATION: (4)
OTHER INFORMATION: n equals a,t,g, or
NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc,feature
LOCATION: (5126)
OTHER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
TITLE OF INVENTION: GENES
CURRENT FILL OF A-0028 US
CURRENT FILLNG DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
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992 GTCTGCTGGCCCTCCAGGCTTCCCAGGTGCCCCTGGCCCCAAGGGTGAAATTGGARCTGT
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OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.13
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51.3%; Pred. No. 9e-18;
tive 0; Mismatches 235;
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ORGANISM: Homo sapiens
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LENGTH: 5432
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PAPELICANT: Weaver, Zoe

TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C

TITLE OF INVENTION: Gene Sets

TITLE OF INVENTION: Gene Sets

FILE REPERRICE: 689230-77

CURRENT APPLICATION NUMBER: US/09/954,531

CURRENT APPLICATION NUMBER: US/60/234,133

PRIOR APPLICATION NUMBER: US/60/234,009

PRIOR PELING DATE: 2000-09-20

PRIOR PELING DATE: 2000-09-20

PRIOR PELING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-20

PRIOR FILING DATE: 2000-09-22

PRIOR FILING DATE: 2000-09-22
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  1963 CACGGCTGGGCCCCCAGGGGTCCCTGGCTCCCTGGAATCACGGGCCCTCC 2022
                                                                                                                    2023 GGGGCCTCCCGGGCCCCCGGGACCCCCTGGTGCCCCTGGGGCCTTCGATGAGACTGGCAT 2082
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                                                                                                                                                                                                                                                                                                                                Sequence 961, Application US/09954531 Patent No. US20020165180A1 GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-09-954-531-961
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APPLICANT: Recipon, Herve
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chenghua
TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and PT
FILE REFERENCE: DEX-0269
CURRENT APPLICATION NUMBER: 05/249,998
PRIOR FILING DATE: 2000-11-20
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 137
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                     1603 AGGCCTGGAGGACCCCCAGGAGTGCCTGGCATTCGAGGTGACCAGGGGCCTAGTGGCCT 1662
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                                                                                                                    186 AACTGGCAACAAGGGACAGAAAGGAGAGAGGGGGAGCCTGGACCACCTGGCCCTGCGGG 245
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420 TCAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGG
                                            1342 CTCCGGCCCCGTTGGACCTCCTGGTAATCCTGGAGCAAACGGCCTTACTGGTGCCAAGGG
                                                                                           ACCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCCAAGGGCCCCCC
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Pred. No. 9.6e-18;
0; Mismatches 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 33, Application US/10001887
Patent No. US20020155464A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Maclina, Roberto
APPLICANT: Reclipon, Herve
APPLICANT: Cafferkey, Robert
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Best Local Similarity 52.9%;
Matches 256; Conservative
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Sequence 255, Application US/09964824A

Sequence 255, Application US/09964824A

Patent No. US20020102531A1

GENERAL INFORMATION:

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

TITLE OF INVENTION: Sets

FILE REFERENCE: 689290-73

CURRENT APPLICATION NUMBER: US/09/964, 824A

CURRENT PILING DATE: 2001-09-27

PRIOR APPLICATION NUMBER: US/60/236, 033

PRIOR PILING DATE: 2000-09-28

PRIOR APPLICATION NUMBER: US/60/236, 032

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

PRIOR FILING DATE: 2000-09-28

SOFTWARE: PatentIn version 3.0

SEQ ID NO 255

LEASTH: 2542
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7.8%; Score 106; DB 10; Length 2
Best Local Similarity 52.1%; Pred. No. 1.1e-17;
Matches 236; Conservative 0; Mismatches 217; Indels
                    1050 GTCCCCCTGGGAAAGAGGGGAGAGCCAGGGCCTC 1082
542 GCCCTCCTGGCCCATCAGGAGCGGTGGTGCCCC 574
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; ORGANISM: Homo sapiens
US-09-964-824A-255
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AL569543 AL569543

R74388 Y15711.s1

BB929813 RC3-GN004

BB749743 BB749743

BB79797 QV1-GN006

AW18393 EST346697

BW77917 QV1-GN006

AA700864 zj36b11.s
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BE910803 601661855
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BQ021066 UI-H-DH1-
A774261 wq44f06.x
AW956637 BST368697
R78202 Y181h07.rl
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 3305)
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Submitted (05-JUN-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wis musculus, Similar to scavenger receptor with C-type lectin, clone IMAGE:2811487, mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: capabbz-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
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BB248064
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AW956633
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AUTHORS
TITLE
JOURNAL
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COMMENT
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                                                                                              March 21, 2003, 01:34:06 ; Search time 1777.64 Seconds (without alignments) 12344.923 Million cell updates/sec
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Copyright (c) 1993
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523.4
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Minimum DB Maximum DB

Database

Result . Ю

Searched:

Sequence:

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TITLE
JOURNAL
COMMENT
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                                                     found
                                                                                                                                                                              /clone="IMAGE:2811487"
//Lssue_type="Mammary tumor. WAP-TGF alpha model. 7 months
old gross tissue,"
                                                                                                                                                                                                                                                                                                5;
                                                  Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov/Series: IRAK Plate: 5 Row: h Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
          Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.
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                                                                                                                 clone has the following problem: incomplete processing.

Location/Qualifiers
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                                                                                                                                                                                                                                                                             Length 3305;
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                                                                                                                                                                                                                                                                           Score 900; DB 11;
Pred. No. 4.5e-173;
0; Mismatches 230;
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                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6"
757 c 760 g 757 t
                                                                                                                                                                                                  old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
Contact: amg@bcm.tmc.edu
Unanzatne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
                                                                                                                                                                                                                                                                          Query Match 66.4%;
Best Local Similarity 81.7%;
Matches 1106; Conservative
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AL568743 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE005YH04 3 prime
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 967)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-Length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                    2015
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                                                                                                                                                            2016 CATCTCGTTTTCATAAACTCAAGAAGAACAGCAATGGATAAAAAAAGCATACCGTGGGG
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AL568743
AL568743.1 GI:12923387
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                                         /note="Organ: Placenta; Vector: pcwVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cLoned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies. Context: Feng Libary Enfonciogies. Technologies. Context: Feng Libary Life Technologies. Context: Feng Libary Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville filangelifetech.com URL:

http://tullegth.invitrogen.com"

221 c 217 g 290 t 17 others
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                                                                                                                                                                                                Length 967;
                                                                                                                                                                                                                        Indels
                                                                                                                                                                                               56.3%; Score 762.4; DB 9; 95.5%; Pred. No. 4.5e-145; ive 13; Mismatches 19;
       /clone="CS0DE005YH04"
/clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
/db_xref="taxon:9606"
                                                                                                                                                                                                           Local Similarity 95.5 es 802; Conservative
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1. .668
/organism="Homo sapiens"
/organism="Homo sapiens"
/dlone="Index 2019606"
/clone="Index 2019606"
/clone="Organ: salidary gland; Vector: porB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhol sites ausing the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1345
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Pred. No. 6.1e-121;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Musina;
I (bases 1 to 861)

RS NIH MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI3721 row: n column: 01
High quality sequence stop: 598.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:6306240"
/clone="ImAGE:6306240"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Organ: olfactory epithelium; Vector:
pCMV-SPORT6.1.cdb; Site_1: EccRV; Site_2: NotI; Cloned
unidlrectionally. Primer: oligo dr. Average insert size
unidlrectionally Primer: oligo dr. Average insert size
is a NHLMGC Library."
is a NHLMGC Library. Invitrogen Corp. Note: this
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861 bp mRNA linear EST 16-JUL-2002
AGENCOURT_8482828 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6306240
5, mRNA sequence.
BQ713873
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                                                                                                                                               ACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTCCAATGTGAAGACGTCAATA
                              GCCTCACAGACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTCCAGACT
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Pred. No. 3.7e-103;
0; Mismatches 132;
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EST.
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82.8%;
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Matches 647; Conservative
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DUUV41/b 723 bp mRNA linear EST 26-MAR-2002 UI-H-EIO-aym-p-04-0-UI.s1 NCI_CGAP_EIO Homo sapiens cDNA clone IMAGE:5840883 3', mRNA sequence.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 723)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATACTACAAGGTCCAC
                                                                                                                                                  CGGGCCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCTGGCCCAACTGGCA
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BQ004176.1 GI:19729076
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01-JUN-2000

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Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
Quackenbush, J.
                                                                                                                                                                                                                                                      AW958053 552 bp mRNA linear EST 01-JUN-200
EST370123 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
AW958053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
                                          694 AAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCATAAACACTAGAGAGAACAG 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 GCTGGACAGCCGGATAACTGGGGTCATGGCCATGGGCCAGGAGAAGACTGTGCTGGGTTG 360
    GGGTGATATGCTGATTTTCATTGTGCACATGGACTGAATCACATAGATTCTCCTCCGTCA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CTGGCCCTGCAGAATGAGCCAACCCCGGCACCGGAGGACAATGGCTGCCCGCCTCACTGG
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Catarrhini; Hominidae; Homo.
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/clone_lib="MAGE resequences, P
/note="Vector: pBluescriptSKm"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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1. .552
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 552)
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                                                                                                                                                                                                                                                                                                                                AW958053.1 GI:8147736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: johnq@tigr.org
Plate: 115
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VERSION
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                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="IMAGE:5840883"
/clone="IMAGE:5840883"
/clone="IMAGE:5840883"
/clone="lib="work_CCGAP_EIO"
/tlssue_type="Chondrosarcoma"
/dev_stage="Adult"
/lab_host="bH108 (Life Technologies)"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
/note="Organ: Left Pelvis; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_EIO is a cDNA library containing the following
tissue(s): Chondrosarcoma. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT7T3-Pac
vector. The ollgonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT18 tail. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
;
                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Extraportion: Clone distribution information can be found
through the I.M.A.G.E. Consortium/Libra dt: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     983 TCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCTGCATTATAACGGACTGTGATGG 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1043 GATCACATGAGCAAATTTTCAGCTCTCAAAGGCAAAGGACACTCCTTTCTAATTGCATCA 1102
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99.5%; Pred. No. 1.9e-96;
iive 0; Mismatches 1.
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TAG_SEQ=ACACTTGCAC"
148 c 130 g 260
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                                                                                                                                                                                                                              Location/Qualifiers
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Unpublished (1997)
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Matches 546; Conservative
                                                                                                                                                                                    Seq primer POLYA-Yes.
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TITLE
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COMMENT
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="TundgE:4616625"
/clone=lib="MHI_MGC_77"
/lab_host="MHI_MGC_77"
/lab_host="MHI_MGC_77"
/lab_host="DHIOB (TT phage-resistant)"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: Sfil (ggecaettaggec); Site_2: Sfil (ggecaettaggec); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATATGGCC-3' and 3' adaptor sequence: 5'-CATGTAGAGGCCGACATG-GT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9
kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                          BG482931 655 bp mRNA linear EST 21-MAR-2001 602502939F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4616625 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                    993 AAAAGACAGGAGACAGTACTGTCATCTGCATTATAACGGACTGTGATGGGATCACATGA 1052
                                                                                                                                                                                       1053 GCAAATTTTCAGCTCTCAAAGGCAAAGGACACTCCTTTCTAATTGCATCACCTTCTCATC 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
High quality sequence stop: 651.
                                                                                                                          361 ATTTATGCTGGGCAGGGGAACGATTTCCAATGTGAAGACGTCAATAACTTTAATTTGCGA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       826 GAATGGAAGTGGCTGGATGGGACATCTCCAGACTACAAAAATTGGAAAGCTGGACAGCCG 885
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NIH *MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1. .655
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BG482931.1 GI:13415210
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Matches
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Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 500)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Program for Rat Gene Discovery and Mapping
University of Iowa
451 Ecstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 956
                                                                                                                                                                                              1006 ACAGTACTGTCATCTGCATTATAACGGACTGTGATGGGATCACATGAGCAATTTTCAGC 1065
                                                                              946 CAGTGGAACGATTTCCAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAG 1005
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                                                                                                                                                                                                                                                                                                                 1066 TCTCAAAGGCAAAGGACACTCCTTTCTAATTGCATCACCTTCTCATCAGATTGAAAAAA 1125
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                                                                                                            241 TCTCAAAGGCAAAGGACACTCTTTCTAATTGCATCACCTTCTCATCAGATG--AAAAA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 AAAAAGCACTGAAAGCCAATTACTGAAAAAAAGGACAGCTAGTGTTTTTACCATCG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418
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/db_xref="taxon:9606"
/clone="UI-E200-ahq-c-05-0-UI"
/clone_lib="UI-E-E10"
/tissue_type="fetal eyes, lens, eye anterior segment,
                                                                                                                                                                                                                                                          181 ACAGTACTGTCATCTGCATTATAACGGACTGTGATGGGATCACATGAGCAAATTTTCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                 1126 AAAAAGCACTGAAAACCAATTACTGAAAAAAAATTGACAGCTAGTGTTTTTACCATCCG
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97044477
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Seg primer: M13 Forward
POLYA=Yes.
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                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
                                                                                                                                                                                                                                                          {\tt Bonalido,M.F., Lennon,G. and Soares,M.B.} \\ {\tt Normalization and subtraction: two approaches to facilitate gene} \\
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         797 TCGGCCTCACAGACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTCCAG 856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA sequence: 443-498, >POLY_A#Simple_repeat
Seq primer: M13 Reverse.
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                                                                                                                                                                                                                                                                                                                                                                                       97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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/clone="UI-E-EJO-ahq-c-05-0-UI"
/clone_lib="UI-E-EJO"
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0; Mismatches 2
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/organism="Homo sapiens"
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                                     GI:19027149
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                                                                                                                                   Homo sapiens
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                                               Jackstage="fetal and adult"

/dev_stage="fetal and adult"

/lab_host="DH10B (Life Technologies) (Tl phage resistant)"

/note="Organ: eye; Vector: pTT3-pac (Fharmacia) with a
modified polylinker: Site_1: ECOR I; Site_2: Not I;

UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dy primer containing a Not I site. Double
stranded cDNA was ligated to an ECOR I adaptor, digested
with Not I, and cloned directionally into pT773-pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGTG; retina, CGCG; Retina Foveal and
Macular, GTC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
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optic nerve, retina, Retina Foveal and Macular, RPE and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 AGGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACATCTTGTTTTCA 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    794 GGATCGCCCTCACAGACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTC 853
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UI-E-EJO-ahq-c-05-0-UI.rl UI-E-EJO Homo sapiens cDNA clone
UI-E-EJO-ahq-c-05-0-UI 5', mRNA sequence.
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Length 906;

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In Unpublished (1999)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov

Plate: LAMI1636 row: b column: 17

High quality sequence stop: 730.

L. 1906

L. 1906
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                                                                                                                                                             977 ATAACTICATITGCGAAAAAGACAGGAGACAGIACTGICATCTGCATIAIAACGGACTG 1036
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                                                          917 AAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTCCAATGTGAAGACGTCA
                                                                                                                                                                            /organism="Mus musculus"
/strain="C57BL/64"
/db_re="taxon:10090"
/clone="IMAGE:521888"
/clone_lib="NOI_CGAP_Mam5"
/tissue="type="tumor, gross tissue"
/dev_stage="T months"
/lab_host="DH108"
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BE910803 580 bp mRNA linear EST 29-SEP-2000 601661855F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:3962292 5', mRNA sequence.
BE910803.1 GI:10407765
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 580)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                             243 CTACAAGGTCCTCCTGGCCCCAGAGGTCCAAAAGGTGACAGAGGATCTCAGGGACCACT
                                                                                                                                                                                                                                                          181 GCCCCAACTGGCAACAAGGGACAGAAAGGAGAGAGGGGGGAGCCTGGACCACCTGGCCCT
                                                                                                                                                                                                                                                                          241 GCGGGTGAGAGGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAGGGTGGCGGCAAAGGA
                                                                                                                                                                                                                                                                                                                                            TCTAAAGGCTCCCAGGGCCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAG
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                                                              1 ATGCAACAAGATTTGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATT
                                                                                                                                                                                              CTACAAGGTCCACCGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCT
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                                Indels
               4.5e-84;
34.1%; Score 462.6;
llarity 81.7%; Pred. No. 4.5e
Conservative 0; Mismatches
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841 AATTTTCCAAT 851
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Matches 597; Conserv
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JOURNAL
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/organism="miscatus"
//organism="miscatus"
//clone_lib="NulH_BMAP_FIO"
//clone_lib="whole brain"
//dev_stage="embryol2:5pc"
//dev
                                                                 BQ771366
UI-M-FIO-byu-g-09-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
Murinae; Mus
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae;
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153 c 161 g 107 t
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                 Email: capbS-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can b
found through the I.M.A.G.E. Consortium/LLNL at:
http://imaqe.llnl.gov
Plate: LLAM9128 row: m column: 13
High quality sequence stop: 580.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       470 GGGTGCCTGGACCTCGGGGACTGCCAGGCTTGCCTGGGGTACCAGGCATGCCAGGCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tch 32.9%; Score 445.6; DB 12; Length 580; al Similarity 85.5%; Pred. No. 1.3e-80; 496; Conservative 0; Mismatches 84; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib-"NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_nost="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              541 GGAAGTGGCTAGACGGGTCACCTGTTGATTACAAAAACTG 580
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                           1. .580 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3962292"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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division of Invitrogen 9800 Medical Center Drive Rockville Maryland 20850, USA Fax : (1) 301 610 8371 Email : Hilang@lifetech.com URL : http://fulllequeh.invitrogen.com" 17 q 201 t 12 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE290299 601 bp mRNA linear EST 26-OCT-2000 601089246F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3484163 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 601)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1149 TGAAAAAAATTGACAGCTAGTGTTTTTTACCATCCGTCATTACCAAAGACTTGGGAAC 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCTGCATTATA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                             457 CCACTGGATCGCCCTCACARACTCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGGCAGTGGAACGATTTCCAATGTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.8%; Score 416.8; DB 989.5%; Pred. No. 9.3e-75;
                                                                                                                                                                                    7; Mismatches
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALS43000 LTI_FL002_PL1 Homo sapiens cDNA clone CSODE013XJ08 3 prime
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualiflers
            241 ACAGGAAAGCGAAAGGGAAGTGGCAAGAAGGGGTCACCTGTTGATTACAAAAACTGGAAAGC
                                                                                                                                                                      876 TGGACAGCCGGATAACTGGGGTCATGGCCATGGGCCAGGAGAGTGTGTGCTGGGTTGAT
                                                                                                                                                                                                                             936 TTATGCTGGGCAGTGGAACGATTTCCAATGTGAAGACGTCAATAACTTCATTTGCGAAAA
                                                                                                                                                                                                                                                                                                     996 AGACAGGGAGACAGTACTGTCATCTGCATTATAACGGACTGTGATGGGATCACATGAGCA
                                                                                                                                                                                                                                                                                                                         421 GGAAAGGGAGGAGTACCATCATCATATAAACAGCATGATAATAGCAGAAACATA
                                                                                                                                                                                                                                                                                                                                                                                 1056 AATTTTCA--GCTCTCAAAGGCAAAGGACACTCCTTTCTAATTGCATCACCTTCTCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1174 TTTTACCATCCGTCATTACCCAAAGACTTGGGAACTAAAATG-TTCCCCAGGGTGATATG
                                                                      GCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTCCAGACTACAAAATTGGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="LTI_FL002_PL1"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="CSODE013YJ08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL543000.1 GI:12875478
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AL543000
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Arkawa, T. Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Lobi, T., Ishi, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Kayai, J., Konno, H., Kouda, M., Koyai, S., Matsuyama, T., Ishi, Y., Ito, M., Kayai, J., Konno, H., Kouda, M., Koyai, S., Matsuyama, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, J., Saibata, K., Shinagawa, A., Shinaki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y. RIKBN Mouse ESTS (Arakawa, T., et al. 2001)

Unpublished (2001)

on Jul 6, 2000 this sequence version replaced gi:8940810.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RÍKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2
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URL:http://genome-ssc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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                                                                 Chordata; Craniata; Vertebrata; Buteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Manm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/dev_stage="7 days neonate"
/lab_host="DH108"
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                                                                                                     Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                          /note-"Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Stle_2: NotI; Clouded unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 AAGGGACAGAAAGGAGAGAGGGGGAGCCTGGACCACCTGCCGGGTGAGAGAGC 255
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                                                                                                                                                                                                                                                                    /clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
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                                                                                                                                     /organism="Mus musculus"
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                                                                                                                                                                  /strain="C57BL/6J"
/db_xref="taxon:10090"
                                High quality sequence stop: 5 Location/Qualifiers
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Search completed: March 21, 2003, 08:08:35 Job time: 1791.64 secs

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Command line parameters:
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-DE-GGNZ_1/USFPC_spool/US9763712/runat_14032003_100949_18091/app_query.fasta_1.1877
-DB=N_Geneseq_101002 -QFNT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=b1ts -STAFT=1 -END=-1 -MATRIX=b1cound2 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE_EFT - THR_MIN--100 -THR_MIN-0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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The invention relates to polynucleotides encoding a new collectin of human origin. The collectin can be used as an antibacterial and antiviral agent and for screening potential drug molecules. The new collectin can be produced by standard recombinant methodology. The present sequence
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(1-2024)US-09-763-712A-2 (1-547) x AAA07697

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The invention relates to a human scavenger receptor-like protein. The protein is useful as a target molecule for diagnosis, prevention and treatment of autoimmune diseases such as rheumatoid arthritis.

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GlnTrpAsnAspPheGlnCysGluAspValAsnAsnPheIleCysGluLysAspArgGlu
                                                   ASPLySCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLysLeuPheCys
                                                                GACAAATGCTACTATTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGT
                                                                             GluAspLysSerSerHisLeuValPheIleAsnThrArgGluGluGlnGlnTrpIleLys
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         1459 GGACCACCTGGCCCTGCGGGTGAGAGGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAG
                                       LysGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsn
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The present sequence encodes a human scavenger receptor, designated STGL-P1. The STGL-P1 polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic compilcations, bacterial infection and restenois following angioplasty, which are associated with accumulation of exidized low density
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                                        "scavenger receptor"
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 79-84; 118pp; Japanese.
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral socierosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemotactic/chemokinetic activity, haemostatic
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Xu C, Xue AJ,
R, Drmanac RT;
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LysProGlyProGlnGlyProSerGlyAspProGlyProProGlyProProGlyLysGlu
                                                                                GlyLeuProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGlu
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                                                                                                                                                                             (INCY-) INCYTE GENOMICS INC
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Percent Similarity: Best Local Similarity: Query Match:

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Alignment Scores:

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WPI; 2001-007395/01. P-PSDB; AAB27236.

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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervopathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral scierosis, and Shy Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibhn activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening,
                                                                                                                                                                                                                                                                                                                               Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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AspAsnTrpGlyHisGlyHisGlyProGlyGluAspCysAlaGlyLeuIleTyrAlaGly
                               GATAACTGGGGTCATGGCCATGGGCCAGGAGAAGACTGTGCTGGGTTGATTTATGCTGGG
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Zhang J;
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Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
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Wang Z, Wehrman T, Xt
Zhou P, Goodrich R,
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25-APR-2000; 2000US-0552117.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-065450.
14-SEP-2000; 2000US-065450.
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P-PSDB; AAM39686.
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assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.
Note: The sequence data for this patent did not form part of the printed
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The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary deoxyribonucleic acid (CDNA) inserts (II), where the protein is substantially free from other mammalian proteins. (I) are useful for preventing, treating or amalogenesis, or preventing a medical condition, especially immunological treatment or prevention of tumours. (I) exhibits activity relating to amalogenesis, cytokine, cell proliferation, call differentiation, antinfiammatory, stem cell growth factor activity and activin or inhibin-related activity relating to amalogenesis, cytokine, cell proliferation, coll differentiation of merval cells and activity and activin or inhibin-related colls and cativities. (I) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or rise to neuroepithelial cells that can be used to augment or replace cells and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzahmer's, Parkinson's disease, amyctrophic certivity, regulation of haematopoiesis and is useful for treating myeloid or lateral sclerosis. (I) is involved in chemotactic or chemokinetic cor lymphoid cell disorders, platelet disorders such as thrombocytopaenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders or periodontal disease. (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune disorders and disorders erg. multiple sclerosis, rhemmatoid arthritis, autoimmune disorders erg. multiple sclerosis, rhemmatoid arthritis, such as asthma or other respiratory problems. (II) is such the corresponding protein is preferentially processed and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autolmmune diseases, bone disorders and lung or liver fibrosis
Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss
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Spaulding V;
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activin/inhibin; chemokinesis; haemostasis; thrombolysis;
receptor/ligand activity; anti-inflammatory; tumour inhibitor;
cadherin/tumour invasion suppressor; ds.
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Indels:
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                                    US-09-763-712A-2 (1-547) x ABQ92072
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This DNA sequence was isolated from a human adult brain cDNA

This DNA sequence was isolated from a human adult brain cDNA

This DNA sequence was isolated from a human adult brain cDNA

This DNA and proteins

Sultable for treating, preventing or ameliorating medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional sources or supplements, immune ctivities include nutritional sources or supplements, immune ctivity, tissue growth activity, activiny, haemacopoiesis regulating activity, is used growth activity, anti-inflammatory activity, cadherin/tumour nvasion suppressor activity, and tumour inhibition activity. The DNAs are also stated to be useful for gene therapy. A host cell transfected with the DNA, or its subfragments and variants is useful for recombinant production of the human secreted protein clones.
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retina, adult placenta or adult uterus c
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                                                                                                                                                                                                                                                                                                                                                                                                                 AAGAATTTTACAATACTACAAGGTCCACCGGGCCCCAGGGGGTCCAAGAGGTGACAGAGGA
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                            CAGATGGAGAACATCACCACTATCTCTCAAGCCAACGAGCAGAACCTGAAAGACCTGCAG
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                                                                                                            PheGlnLeuPheGluThrAspIleValAsnIleIleSerAsnIleSerTyrThrAlaHis
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                                                                                                                                                                                                                                                                                                                                    Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
low density lipoprotein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence encodes a human scavenger receptor, designated SRCL-P1. The SRCL-P1 polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic complications, bacterial infection and restenosis following angioplasty, which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for treatment and diagnosis of diseases associated with oxidized low-density lipoprotein accumulation
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                                          2031 AAACAGATGGTAGGGAGAGAGAGCCACTGGATCGGCCTCACAGACTCAGAGCGTGAAAAT
                                                                                                           2151 GATAACTGGGGTCATGGCCATGGGCCAGGAGAACACTGTGCTGGGTTGATTTATGCTGGG
LysGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsn
                                                                                      AspAsnTrpGlyHisGlyHisGlyProGlyGluAspCysAlaGlyLeuIleTyrAlaGly
                                                                                                                                 GlnTrpAsnAspPheGlnCysGluAspValAsnAsnPheIleCysGluLysAspArgGlu
                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a human scavenger receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "scavenger receptor"
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2000JP-0309068
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 other;
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25-JUL-2000; 2000US-220654P.
28-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
28-JUL-2000; 2000US-220664P.
27-AUG-2000; 2000US-2206595P.
27-AUG-2000; 2000US-0643657.
27-AUG-2000; 2000US-053328.
27-AUG-2000; 2000US-23097RP.
18-SEP-2000; 2000US-23097RP.
18-SEP-2000; 2000US-0665350.
24-OCT-2000; 2000US-0665350.
24-OCT-2000; 2000US-065350.
24-OCT-2000; 2000US-065350.
24-OCT-2000; 2000US-065350.
24-OCT-2000; 2000US-0709238.
01-DEC-2000; 2000US-0730952.
01-DEC-2000; 2000US-0730953.
01-DEC-2000; 2000WO-US30952.
01-DEC-2000; 2000WO-US30952.
01-MAR-2001; 2001US-076666.
09-MAR-2001; 2001US-086669.
25-MAR-2001; 2001US-0866028.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-0866034.
25-MAY-2001; 2001US-08646034.
25-MAY-2001; 2001US-08646034.
25-MAY-2001; 2001US-08646034.
25-MAY-2001; 2001US-0866028.
20-JUN-2001; 2001WO-USJ19602.
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FERRARA N.
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  Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
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2237 CAGTGGAATGACTTCCAGTGTGATGAAATCAATAACTTCATTTGTGAGAAGGAAAGGGAG
                                 LysProGlyProGlnGlyProSerGlyAspProGlyProProGlyProProGlyLysGlu
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PA (GERH,) GERETRER N.)
PA (GODD,) GODDARD A.
PA (GODD,) GODDARD A.
PA (GODD,) GODDARD A.
PA (GURL,) HILLAN K J.
PA (HILL,) HILLAN K J.
PA (WATE,) MARSTERS S A.
PA (WATE,) MARSTERS S A.
PA (WATE,) WALBEC K.
PA (WALL,) WALLIAMS P M.
PA (WALL,) WOOD W I.

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PI (GODOWSKI PY, GURNEY AL, Hillan KJ, MARSTERS SA, Pan J, Paoni NF;
PI (Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
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Cone hundred and eighty English.
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Claim 1; Fig 27; 567pp; English.
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CC The present invention provides the protein and coding sequences of human CC The present invention provides are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac
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arthritis,
       atherosclerosis, hypertension, arterial restenosis, rheumatoid arthrit. anglor myocardial infarctions, thrombophebitis, lymphangitis, tumour anglogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
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 age-related macular degeneration,
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99.60%
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Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; andothelial disorder; cancer; anglogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; hymbhangitis; tumour anglogenesis; breast carcinona; lymphangitis; tumour anglogenesis; breast carcinona; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
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L, Hillan KJ, Marsters SA,
CK, Williams PM, Wood WI,
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            2000US-220624P.
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                                                                                                                  SerProAspTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGly
                                         GluLysGluIlePheGluAspAlaLysLeuPheCysGluAspLysSerSerHisLeuVal
                                                                                                                                                                                                                                         Nucleotide sequence of a human scavenger receptor
                                                                                                                                                                                                                                                                                                            receptor"
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                                                                                                                                                                                                                                                                                                           /product= "scavenger
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The present sequence encodes a human scavenger receptor, designated SRCL-Pl. The SRCL-Pl polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal mimunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, diabetic complications, bacterial infection and restenosis following angioplasty, which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products into cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AspTrpLeuLysGluLysValGlnSerLeuGlnThrLeuAlaAlaAsnAsnSerAlaLeu
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Matches:
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food supplement; medical imaging; diagnostic; genetic disorder;
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1379 AAGAATTTTACAATACTACAAGGTCCACCGGCCCCCAGGGGTCCAAGAGGTGACAGAGGA 1438
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                                                                                         321 LysProGlyProGlnGlyProSerGlyAspProGlyProProGlyProProGlyLysGlu 340
                                                                                                                   341 GlyLeuProGlyProGlnGlyProProProGlyPheGlnGlyLeuGlnGlyThrValGlyGlu 360
                                                                                                                                                                       381 ProLysGlyProProGlyProProGlyProSerGlyAlaValValProLeuAlaLeuGln 400
                                                                                                                                                                                                                                                                               LysGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsn 480
                                       GlyProProGlyProAlaGlyGluArgGlyProIleGlyProAlaGlyProProGlyGlu 300
                                                                                                                                                                                                                                                                                    361 ProGlyValProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGly
                                                                                                                                                                                                AsnGluProThrProAlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThr
                                                                                                                                                                                                                           AspLysCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLysLeuPheCys
                                                                ArgGlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGly
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                                                                             novel human diagnostic protein #6937.
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags of orientifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantificating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in capposition for generic disorders or other trails to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Camino acid sequences AAS64197-AAS94564 represent novel human by and diagnostic coding sequences of the invention.

Cappositication, but was obtained in electronic format directly from WIPO
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2000US-0649167.
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Best Local Similarity:
Query Match:
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23-AUG-2000;
Homo sapiens
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ProProGlyProAlaGlyGluArgGlyProIleGlyProAlaGlyProProGlyGluArg
       GlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLys
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This sequence encodes the human cellular stress response 3 (CSR3) protein of the invention. The CSR proteins are macrophage scavenger receptor proteins. The CSR proteins can be used in the treatment, gene therapy and diagnosis of diseases in which intracellular stress is important, such as arteriosclerosis, diabetic circulatory obstruction, and microbial infection. Expression of the proteins is induced in vivo in response to intracellular stress, and inhibits cell death as a result of such stress.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  808 GTGCACCAGATCAACTTCACCGTGGGGCAGACTTCCGAGTGGATCCACGGGATCCAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerValAspAspThrSerGlnAlaIleGlnArgIleLysAsnAspPheGlnAsnLeuGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51 GlnValPheLeuGlnAlaLysLysAspThrAspTrpLeuLysGluLysValGlnSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 Gln---ThrLeuAlaAsnAsnAsnSerAlaLeuAlaLysAlaAsnAsnAspThrLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 GlnAlaAsnGluGlnAsnLeuLysAspLeuGlnAspLeuHisLysAspAlaGluAsnArg
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                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                    proteins - for treatment and diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 901 A; 1142 C; 972 G; 669 T; 1 other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                         Japanese.
                                                                                                                                                                                                                                                                                                        Scavenger receptor proteins - for disorders involving cell stress
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765.00
60.41%
39.59%
25.77%
                                                                                98JP-0230121
97JP-0233396
                                        98WO-JP03602
                                                                                                                                                     NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                             Tokino T;
                                                                                                                                                                                                                                        WPI; 1999-181032/15.
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                P-PSDB; AAY00994
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                                                                                  30-JUL-1998;
13-AUG-1997;
                                        12-AUG-1998;
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25-FEB-1999
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1585 GGCAGAGGCCCGAAAGAGAGACCCCGGCATCTTGGGCCCCCTGGGACCCCAGGGTCCTCAG 1644
                                                                                                                                                                                                        -----GGACAGCCAGGCCCAAAAGGGGACATAGGGCCCCCAGGGCCCAGAAGGCCCCCG 1806
                                                                                                                                                                                                                                                                                                                                    GGGTCTCCAGGGCCTCAGGGCAAAACCGGGAATTGCAGGGAAGACAGGGTCA 1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cellular stress response protein; CSR1; CSR2; CSR3; human; macrophage;
                                       CIGAACAAGICTGCTCCATCATGCTGGGCACCACAGAACCTGCTCCGGGAGGGCTTCAGC 1404
                                                                                                           LysLeuValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyPro 249
                                                                                                                                                                     AsnLysGlyGlnLysGlyGlu-----Lys 277
                                                                                                                                                                                                                                              317
                                                                                                                                                                                                                                                                                                                    GlyLysGluGlyLeuProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThr 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scavenger receptor protein; intracellular stress; arteriosclerosis; diabetic circulatory obstruction; microbial infection; ss.
                                                                       LeuMetArgSerArgLeuAspThrGluValAlaAsnLeuSerValIleMetGluGluMet
                                                                                                                                                                                                                                            ProGlyGluArgGlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGly
                                                                                                                                                                                                                                                                                SerProGlyLysProGlnGlyProSerGlyAspProGlyProProGlyProPro
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                          LeuAsnAsnThrLeuAlaAsnIleArgLeuAspSerValSerLeuArgMetGlnGlnAsp
                                                                                                                                                                                                                                                       MetProGlyProLysGlyProProGly 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CSR1 protein coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX27856 standard; DNA; 3810 BP
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13-AUG-1997;
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This sequence encodes the human cellular stress response 1 (CSR1) protein of the invention. The CSR proteins are macrophage scavenger receptor proteins. The CSR proteins can be used in the treatment, gene therapy and diagnosis of diseases in which intracellular stress is important, such as arterioscierosis, diabetic circulatory obstruction, and microbial infection. Expression of the proteins is induced in vivo in response to intracellular stress, and inhibits cell death as a result of such stress.
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COSTCTTCAGCGGCCTGCGCACCACCTCCAAGACTGGAGAGGCGGTCAAGAACATC
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                                                                                                                                  diagnosis
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                              Claim 4; Page 119-127; 175pp; Japanese.
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                                                                                                                                  Scavenger receptor proteins, for disorders involving cell stress
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Tokino
                                                   WPI; 1999-181032/15
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                                                                               P-PSDB; AAX00992
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1530 CTGCTCAGTGCCCGGCTGGACCTCAACGTCCGGAACCTCCTCCATGATCGTGGAGGAGATG 1589
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1710 GGCAGAGGCCCGAAAGGAGACCCCGGCATCTTGGGCCCCCTGGGACCCCCAGGGTCCTCAG 1769
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|830 CCAGGCCTCAAAGGCTCAAAGGCACTTTGGAACTGGAGGGCCGAGA------ 1877
                                                                                                                                                                               278 GlyGluProGlyProProGlyProAlaGlyGluArgGlyProIleGlyProAlaGlyPro 297
                                                                                                                                                298 ProGlyGluArgGlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGly 317
                                                                                 270 AsnLysGlyGlu-----Lys 277
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Search completed: March 21, 2003, 08:37:40 Job time : 318.244 secs

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Sequence 5, Appli
Sequence 1, Appli
Sequence 40, Appli
Sequence 62, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
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APPLICANT: CAPPELLO, Joseph
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SECHENCES: 135
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REALABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/08/642,255
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: FLEER, HOHBACH, TEST, ALBRITTON & STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco CTATE: California COUNTRY: USA
US-09-167-364-1

US-09-449-897-1

US-09-448-970-4

US-09-029-348-20

US-09-249-200-5

US-09-249-200-5

US-09-453-702B-264

US-09-453-702B-264

US-09-453-702B-264

US-09-453-702B-264

US-09-453-702B-1

US-08-392-367B-1

US-08-392-367B-1

US-08-392-367B-1

US-08-393-364-1

US-08-393-364-1

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US-08-393-367-1

US-09-111-470-3

US-09-111-470-9

US-09-453-702B-165

US-09-453-702B-115

US-09-453-702B-115

US-09-453-702B-115

US-09-453-702B-115

US-09-453-702B-117-1

US-09-453-702B-117-1

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US-09-453-702B-117-1

US-09-448-322-1
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ATTORREY/AGENT INFORMATION:
NAME: ROWLAND, BETTEAM I.
REGISTRATION NUMBER: 20,015
REFRENCE/DOCKET NUMBER: A5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8771
TELEFAX: (415) 494-8771
TELEFAX: (115) 494-8771
INFORMATION FOR SEO ID NO: 60:
SEQUENCE CHARACTERISTICS:
    ZIP: 94111-4187
    RESULT 1
US-08-642-255-60
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-Q=Cqqn2_1/CyrpCo_spool/VG050763712/runat_14032003_100951_18187/app_query.fasta_1.1877
-Q=Cqqn2_1/CyrpCo_spool/VG050763712/runat_14032003_100951_18187/app_query.fasta_1.1877
-LOOPEXT=0 -UNITS-bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DGCALIGN=200 -THE_SCORE=PCt -THR_MAR=100 -TRANS=human40.cdi
-LIST=45 -DGCALIGN=200 -THE_SCORE=PCt -THR_MAR=100 -TRRANS=0 -LIST=0000000000
-USER=USO9763712_CGCAL_1008_Grunat_14032003_100951_18187 -NGPU=6 -TCPU=3
-NOX-LDXY -NO_MAAP -LARGEQUERY -NGC_SCORES=0 -WAIT -LONGLOG -DEV_TIMEDUT=120
-WARN_TIMEGUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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2886.622 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
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Copyright (c) 1993 - 2003
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Listing first 45 summaries
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Xgapop 10.0, Xgapext
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Mismatches:
Indels:
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333 EARLE OVINGTON BOULEVARD
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                                                       ; DESCRIPTION: /desc = "synthetic" US-08-642-255-60
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Patent No. 5821089
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APPLICANT: BUECHTER, DOUGLAS
APPLICANT: ZHANG, GUNGHUI
APPLICANT: CONNOLLY, KEVIN
NUMBER OF SEQUENCES: 5
6.52e-18
459.50
53.16%
48.95%
15.48%
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CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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Mismatches:
Indels:
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                                                                                                                     APPLICATION NUMBER: US/08/655,086
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S.
REGISTRATION NUMBER: 32,063
REFERENCE/POCKET NUMBER: 203-1632
TELECHMUNICATION INFORMATION:
TELEPHONE: 516-228-8484
TELEFAX: 516-228-8516
                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                         TELEFAX: 516-228-8516
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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452.50
52.11%
46.48%
15.24%
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TYPE: nucleic acid
STRANDEDNESS: single
ZIP: 11553
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: unknown
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OTHER INFORMATION:
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Best Local Similarity:
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US-09-029-348-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuAspThrGluValAlaAsnLeuSerValIleMetGluGluMetLysLeuValAspSer
                                                                                                                                                                                                       APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: A Embarcadero Center, Suite 3400
CITY: San Francisco
STRATE: California
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99
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                   1481 CCAGGTGAAGCAGGCAAACCTGGTGAACAGGGTGTTCCT 1519
                                                              Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                          Sequence 50, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 3555
TELECOMMUNICATION INFORMATION:
TELEPAX: (415) 494-8771
TELEPAX: (415) 494-8771
TELERX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
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448.50
52.70%
44.59%
15.11%
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MEDIUM TYPE: Floppy disk
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TYPE: nucleic acid
STRANDEDNESS: double
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Query Match:
                                                                                                                                                                                                                                                                                                                                                                        USA
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255 ProArgGlyAspArgGlySerGlnGlyProProGlyProThrGlyAsnLysGlyGlnLys 274
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                                                                                                                      315 SerArgGlySerPro-----GlyLysProGlyProGlnGlyProSerGlyAspPro
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|-----CCGCCAGGTGCGCCTGGACCGGCTGGT
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Patent No. 6771827
GENERAL INFORMATION:
APPLICANT: THE VICTORIA UNIVERSITY OF MANCHESTER;
TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: d0878578US LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT PILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
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Matches:
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                                                                                                      -------AlaGlyGluArgGlyProIleGlyProAla 295
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327
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598 CIGCCTGGTATCGCTGGTCACCATGGTGATCAAGGTGCTCCTGGCTCGTGGGTCCTGCT 657
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                                                          238 CAGTATGAAAAAGAATTGGACTTGGCCCTGGACCAATGGGCTTAATGGGACCTAGA
                                          275 GlyGluLysGlyGluProGlyProProGlyPro------
                                                                                                                                                                                                                      412 Cys---ProPro-----HisTrpLysAsnPheThrAspLysCys 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 GlyProProGlyProProGlyProSerGly------
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ZIP: 0110-2804
COMPUTER READABLE FORM:
WEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08159784 Patent No. 5643783 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Massachusetts
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US-08-159-784-1
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1027 GGACCTCAGGGGCCACCAGGGAAGGATGGCACTCCAGGAAGGGATGGTGAACCGGGTGAC 1086
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Matches:
Conservative:
Mismatches:
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                                                          00246/170001
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ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
REGISTRATION NUMBER: 29,066
REFRENCE/DOCKET NUMBER: 0024/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 GlyProArgGlyPro-----
                                                                                                                                                                                                                                                                                                                                       428.00
46.41%
40.08%
14.42%
                                                                                                                               TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
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943 CCCGCTAGAAACTGCAGAGACCTGAAATTCTGCCATCCTGAACTCAAGACTGGAGATAC 1002
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                                                                                                             ---ArqGlyLeuProGlyLeuProGlyValPro 376
                                           655 CCACCAGGGCCTCGAGGTAACAGAGGTGAAAGAGGATCTGAGGGGTCCCCCAGGCCACCCA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     473 LeuThrAspSerGluArgGluAsnGluTrpLysTrp------LeuAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Brewton, Richard G.
APPLICANT: Mayne, Richard
TITLE OF INFORMATION:
TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                              ProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAsp------
                                                                                                                                                                                                                                                                                                                                                  422 ---LysCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLys-
                                                                                                                                                                                                                                                                                                                                                                                                                                         -----LeuPheCysGluAspLys-----
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PAPLICATION NUMBER: US/08/555,669
FILING DATE: 13-NOV-1995
CLASSIFICATION: 435
                                                                                                                                                                          393 AlaValValProLeuAlaLeuGlnAsnGlu--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8389-030
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08555669 Patent No. 5773248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 836
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEPAX: 415-87-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Halluin, Albert
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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STATE: New York
  363 ValProGlyPro-
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                                                                                                                                                                   APPLICANT: GALANIS, Maria
APPLICANT: RAMSHAW, John A.M.
APPLICANT: RAMSHAW, John A.M.
APPLICANT: RAMSHAW, John A.M.
APPLICANT: RAMSHAW, John A.M.
APPLICANT: MERKMEISTER, Jerome A.
TITLE OF INVENTION: HELICAL PROTEIN, AND YEAST HOST CELLS USEFUL IN SAID
TITLE OF INVENTION: METHOD (As Amended)
TITLE OF INVENTION: METHOD (As Amended)
FILE REFERENCE: Q54004
CURRENT APPLICATION NUMBER: US/09/297,269
CURRENT APPLICATION NUMBER: P03310
EARLIER APPLICATION NUMBER: P04306
EARLIER PILING DATE: 1996-10-29
EARLIER PILING DATE: 1996-110-29
EARLIER PILING DATE: 1996-110-29
EARLIER FILING DATE: 1996-110-29
MUMBER OF SEQ ID NOS: 43
SUDMERE: PATEUN NUMBER: PCT/AU97/00721
EARLIER FILING DATE: 1996-12-19
SEARLIER FILING DATE: 1996-10-29
SUDMERE: PATEUR FILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 ValIleMetGluGluMetLysLeuValAspSerLysHisGlyGlnLeuIleLysAsnPhe 243
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GGGCCAGTTGGACCCCCAGGACCTCCAGGGCCTCCAGGGCCACCAGGACCA 1665
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1119
25
108
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Collagen Type III Alpha I Chain
US-09-297-269-39
                                                                                 Sequence 39, Application US/09297269 Patent No. 6451557 GENERAL INFORMATION: APPLICANT: VAUGHAN, Paul R.
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424.50
42.48%
35.10%
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LENGTH: 1572
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                                           RESULT 6
US-09-297-269-39
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DB:
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		Db 18	П	+	Oy 5 Db 20	RESULT US-09-0 ; Seque ; Paten	GENE	N 00		8	) ; ;		; AT	TE	; ;	SE		FE	0-60-SN ;
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			251 1030	271 1090	291 1150	309	313 1270	333 1330	353 1390	360	360	1510	377 1570	378	1630	378	1690	391 1750	403
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	m		nGlyProProGly            -GGTGCTCCGGGA	oThrGly#      SAAAGGCC	yGluArgo	sGlyser:         sggcrcac	-GlnGlyProLys         CCAGGGCCAGAAG	ASSPETOC             GACGTGC	oglyPheG      AGGTTCCG	CAAAGGAG		PACCAGCG	SGTGTTC		CATCAGGG		AAGGAAGC	ProglyP 	CCCACTG
	2543 121 e: 26 91 176		leLeuGlı	roglyPro	roAlaGly   :::   CCTCTGG	lyserby:     ccaccg	GAGGCTTK	roserGly    TCCGAGG	lyProPro    GTATTGC2	TCGGACCC		CCAACGG	lyLeuPro   :::     scgrccc		AGCAGCG		CGCACCTA	roGlyPro 	ACCGCGG
•	Length: Matches: Conservative Mismatches: Indels: Gaps:	(1-2543)	PheThrI	GlyProP       GGACGAG	ProGlyP       GCCGGCC	GlyLysG      GAGGCTG	GGTGTCC	GlnGlyP           CAGGGCC	ProGlnGL        GACCAGGG	GGCCTGG	1	CAGGGTC	LeuProG		GCCAGCG	1 1 1 1 1 1 1 1 1	TAGCCG	GlyProP	uPro      CCCGGAT
	Length Matche Conser Mismat Indels Gaps:	5-669-11	leLysAsr :::    GTCGCAAC	lyserGlr     ccrccc	roglyPro     TGGGTGAQ	luArgGly            AGCGCGGI	GAGCCCCT	roGlyPro 	euProGly     CTAAGGGA	3TCCCAGC		AAGGCACC	roArgGly     TCTGGGC		SGAAGGAG	1 1 1 1 1 1 1 1	PTGCACAG	lyProLys         srccAGCT	SInAsnGl :::::: SAGGACCC
u.	56-15 .00 598 308 118	x US-08-555	ValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProProGly :::    :::	ProArgGlyProArgGlyAspArgGlySerGlnGlyProProGlyProThrGlyAsnLyS :::	GlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGlyPro	IleGlyProAlaGlyProProGlyGluArgGlyGlyLysGlySer	GCCTCGGCCCACAAGGCCCTCCGGAGCCCCTGGTGCCGAGGCTTCCAGGGCCAGAAG	GlySerargGlySerProGlyLysProGlyProGlnGlyProserGlyAspProGlyPro	ProGlyProProGlyLySGluGlyLeuProGlyProGlnGlyProProGlyPheGlnGly	LeuginglythrValglyglu		GGCAGTCGAGGGAGCTGGGCCCCAAAGGCACCCAGGGTCCCAACGGCACCAGCGGTGTT	ProGlyValProGlyProArgGlyLeuProGlyLeuProGlyValProGly	1	atcacgeggaagccgggagttccggggaaggaggccagcgagcagcgcatcagggagctg	1 1 1 1 1 1	TGTGGGGGATGATCAGCGAACAAATTGCACAGTTAGCCGGGGCACCTAAGGAAGCCTTTG	GCACCCGGGTCCATTGGTCGGCCCGGTCCAGCTCGCCCCTGGGCCCCCAGGACCCCA	Glyalaval-valproLeualaLeuGlnasnGlupro
S: unknown unknown :: cDNA CDS 472098	3.8 419 35. : 29. 14.	(1-547) x t	SHisGly	coArgGl)	yGluLys      cagagc	aGlyPro	ACAAGG	ySerPro    AGACCC	OGlyLys      AGGTGCC	rvalgly      TAAAGG		GGAGCTO	oglyval        cgggccc		יפככפפפי		GATCAGO	CATTGG	alProLe     TCACCCT
un PE: CD	res: arity: nilarity		AspSerLy	ArgGlyPr AGGGCCC	1nLysG]	llyProal	TOGGCCC	SerArgG]     GCATGG	31yProPr        3GTCCGG	LeuGlnGlyThrValGlyGlu           CTTCCTGGGGATAAAGGAGAA		GTCGAGG	II GTGTGCC		CGGGGAA	1	GGGGGAT	CCGGGTC	laval-v :::::  ccarrgg
STRANDEDNESS TOPOLOGY: u MOLECULE TYPE: FEATURE: NAME/KEY: C LOCATION: 4	ot Scor	33-712P	232 ValA :::  986 CTCG								360			378 Met-		8,			
, MOI ; FEE	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match:	US-09-763-712A-2	Oy 2:	Oy 252 Db 1031	Qy 272 Db 1091	Qy 292 Db 1151	Oy 310 Db 1211	Oy 314 Db 1271	Qy 334 Db 1331	Oy 354 Db 1391	0у 36	Db 1451	Oy 361 Db 1511	Qy 37	Db 1571	Qy 378	Db 1631	Qy 379 Db 1691	Qy 392 Db 1751

ΟŻ	404	ThrProAlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAs 421	
qq	1811	CTGGGAGCCCGGGCCCAGAG 1832	2
Qy	421	pLysCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGl 441	
qq	1833		6
δλ		uAspLysSerSerHisLeuValPheIleAsnThrArgGluGluGluGlnTrpIleLysLy 461	
q	1860	1874	4
Οy	461	sGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGl 481	
qq	1875		7
. Оу	481	uTrpLysTrpLeuAspGlyThrSerProAspTyrLysAsnTrpLysAlaGlyGlnProAs 501	
qq	1913	CCCCAAGGC-GTGCCGGCACCAGCAGGACGCCAGGACGGTGCTCCCGGCGAGCCTGG 1971	1
Qγ	501	pAsnTrpGlyHisGlyHisGlyProGly510	
qq	1972	GCCTCCCGGAGATCCTGGGCTTCCAGGTGCCATTGGGGCCCCAGGGGACACCGGGGATCTG 2031	П
Qy	511	GluAspCysAlaGlyLeuIleTyrAlaGly 520	
qq	2032	GCCGTGTTAGGA	
RESULT US-09-	JLT 8 9-073-	LT 8 9-073-663-11 quence 11, Application US/09073663	
Pč	tent N		
	APPLI	APPLICANT: Brewton, Richard G. APPLICANT: Mayne, Richard	
	TITLE		
	CORRE	;	
	STR	ADDRESSEE: McGregor & Adler, LLP STREET: 8011 Candle Lane	
	CIL		
	STA	STATE: Texas COUNTRY: USA	
٠.	ZIP	7071	
	COMPUTER	FER READABLE FORM: IUM TYPE: Floppy disk	
	COM	PUTER: Apple Macintosh	
	SOF	OPERATING SISTEM: MACINIOSN OS 8.1 SOFTWARE: Microsoft WORD for Macintosh	
	CURRE	RRENT APPLICATION DATA: APPLICATION NIMBER: 118/00/2013 663	
٠.,	FIL		
	CLA. ATTORI	CLASSIFICATION: TORNEY/AGENT INFORMATION:	
	NAM	NAME: Benjamin Aaron Adler, Ph.D., J.D.	
	REF	ISTRATION NUMBER: 35,423 GRENCE/DOCKET NUMBER: D5913D	
	TELEC	TELECOMMUNICATION INFORMATION:	
	TEL	IELEFHONE: (/13) //-2321 TELEFAX: (713) 777-6908	
т	NFORMA	FION FOR SEQ ID NO: 11:	
	LEN	Coence Connection 51105. LENGTH: 2543 base pairs	
	TYPE: STRAN	nucleic DEDNESS:	
	TOP	nku	
٠.,	FEATURE		
۰. ۰.	NAME/KEY: LOCATION:	3/KEY: CDS MTION: 472098	
110-0	0-073-4	ř	

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STRANDEDNESS:
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                                  248 GlyProProGlyProArgGlyProArgGlyAspArgGlySerGlnGlyProProGlyPro
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                                                                                                      268 ThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProProAlaGly
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Patent No. 5643783
GENERAL INFORMATION:
APPLICANT: Bjorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE 3.9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
US-09-763-712A-2 (1-547) x US-08-642-255-48 (1-432)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 00246/170001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            388 ProGlyProSerGlyAlaValValPro 396
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FILING DATE: December 1, 1993
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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1003 GGCCCCCCAGGCCCCCTTCATTTCCTGGCCAGGCAGACTATCAGGTTCCGGGG 1062
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706 GGCCCCCCGGACCACCAGGGCAGTTTCGTTTGACTTTCTTCAGAAGGAGGCTGAAATG 765
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                                                                                                                                                                                                                   261
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246 Church Street
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Patent No. 5424408
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T., Morrison, Karen E.,
APPLICANT: G.
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen
TITLE OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 800K storage
                                                                                   Conservative:
Mismatches:
Indels:
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                                                       Length:
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STATE: Conn
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Query Match:
                                                                                       Percent Similarity:
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                                    Alignment Scores:
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US-08-159-784-4
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344 GlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyVal 363
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; Patent No. 5973120;
; GRNERAL INFORMATION:
; APPLICANT: Needers, Stephen T
; APPLICANT: MOITISON, Raren E
; APPLICANT: Hudson, Billy G
; TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
; FILE REFERENCE: 951263A
; CURRENT APPLICATION NUMBER: US/08/399,889B
; CURRENT APPLICATION NUMBER: 07/621091
; EARLIER APPLICATION NUMBER: 07/621091
; EARLIER FILING DATE: 1990-11-30
; NUMBER OF SEQ ID NOS: 25
; NUMBER OF SEQ ID NOS: 25
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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LENGTH: 1416
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172 CCTCCAGGGAGTCCTGTAGAAGGCATAAAAGGAGACAAGGGGTTGATGGGAGAGCCTGGC 231
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103
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                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION 424
PRIOR APPLICATION DATA: No. 5424408 applicable
ATTORNEY/AGENT INFORMATION:
NAME: Barth, Richard S.
REGISTRATION NUMBER: 28180
REGISTRATION NUMBER: 900983/RB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
TELEPHONE: (212) 972-1400
TELEPHONE: (212) 370-1622
TELEPHONE: 123 370-1622
TELEPHONE: 1416 base pairs
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1416 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PUBLICATION INFORMATION: No. 5424408e
US-07-621-091G-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: KMC15
POSITION IN GENOME: NO. 5424408 known
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/621,091G
FILING DATE: 11/30/90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear
MOLECULE TYPE: CDNA tO MRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
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STRAIN: Unknown
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Best Local Similarity:
Query Match:
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172 CCTCCAGGGAGTCCTGTAGAAGGCATAAAAGGAGACAAGGGGTTGATGGGAGAGCCTGGC 231
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                                                                        302 GlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLys
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Patent No. 6007980

GENERAL INFORMATION

APPLICANT: Reeders, Stephen T

APPLICANT: Hudson, Maren E

APPLICANT: Hudson, Billy G

TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides

FILE REFERENCE: 951263B

CURRENT FILING DATE: 1998-10-07

EARLIER TILNG DATE: 1998-10-07

EARLIER TILNG DATE: 1998-10-07

NUMBER OF SEQ ID NOS: 2.0
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LOCATION: (1)..(1416)
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                                  Matches:
Conservative:
Mismatches:
Indels:
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Patent No. 6277558
GENERAL INFORMATION:
     1.69e-14
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                                                    Percent Similarity:
Best Local Similarity:
Alignment Scores:
Pred. No.:
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US-09-439-897-1
                                                                                         Query Match:
                 No.:
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267 ProThrGlyAsn-------LysGlyGlnLysGlyGluLysGlyGluProGly 281
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APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REPERENCE: 95-1263-C
CURRENT APPLICATION NUMBER: US/09/439,897
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1416
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Conservative:
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US-09-439-897-1
                                                                                                                                                                TYPE: DNA ORGANISM: Bos taurus
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Best Local Similarity:
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LOCATION: (1).
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                   APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Mayne
APPLICANT: Walker: Michael G
APPLICANT: Walker: Michael G
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
                                                                                                                                       Sequence 4, Application US/09484970B Patent No. 6426186 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No.
460 LysLysGlnMetValGlyArgGlu-
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400.50
54.89%
48.91%
13.49%
                                                       478 ArgGluAsnGluTrpLys 483
                                                                                  861 CCTGGGAACACTTGGCAG
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                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
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US-09-484-970B-4
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- Search completed; March 21, 2003, 12:34:04 Job time: 73.1137 secs

Perfect score:

Sequence:

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sequence 762, App
Sequence 3046, App
Sequence 2094, Ap
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Sequence 206, App
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Sequence 22, Appl
Sequence 27, Appl
Sequence 448, App
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Sequence 1138, Appl
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Treacy, Maurice
Spaulding, Vikki
INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                0 US-09-880 107-3685

0 US-09-880 107-3685

0 US-09-913-343-1516

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US-10-001-887-33
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STREET: 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENCODING THEM
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Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 198, Application US/09745763 Patent No. US20020065394A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jacobs, Kenneth
MCCoy, John M.
LaVallie, Edward R.
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       O
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"MODEL=frame+_pzn.model -DEV=xlp

"MODEL=frame+_pzn.model -DEV=xlp

"C-cgnz_1/USPTO_Spool/US09763712/runat_14032003_100950_18119/app_guery.fasta_1.1877

-DE-published_Applications_NA -OFWT=fastap -SUFFIX=rnpb -MINNATCH=0.1

-LOOPEXT=0 -LOOPEXT=0 -UNITS=-bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100

-THR_MIN=0 -ALIGN=15 -MODE=LCCAL -OUTFWT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0

-THR_MIN=0 -ALIGN=13 -NO_END=CCAL -OUTFWT=pto -NORM=ext -HEAPSTZE=500 -MINLEN=0

-NCFU=0 -NORUS -NO_MMAP -LARGEQUERY -NO_CSCORES=0 -WAIT -LONGLOG

-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPDP=10 -XGAPBXT=0.5 -FGAPDP=6

-FGAPEXT=7 -YGAPDP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 2274, Ap
Sequence 57, Appl
Sequence 57, Appl
                                                                                                                                                                         March 21, 2003, 08:23:12; search time 265.779 seconds (without alignments) 1596.010 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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                             GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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Maximum Match 100%
Listing first 45 summaries
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Fgapop 6.0 , Fgapext
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Database :

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Matches:
Conservative:
Mismatches:
Indels:
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NT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                         NO: 198
                                                                                                                                                                                                                                      Gaps:
                                             NAME: Sprunger, Suzanne A.
REGIZRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPHONE: (617) 876-5851
SEQUENCE CHARACTERISTICS:
LENGTH: 293 obsee pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                        DESCRIPTION: SEQ ID
                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                         9.15e-151
2936.00
99.63%
99.63%
                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                               MOLECULE
                                                                                                                                                        SEQUENCE
                                                                                                                                                               US-09-745-763-198
                                                                                                                                                                                Alignment Scores:
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383 GlyProProGlyProProGlyProSerGlyAlaValValProLeu---AlaLeuGlnAsn 401
                                            820 GGAGAAAGTGGGCTTCCAGATGTTGCTTCTCTGAGGCAGCAGGTTGAGGCCTTACAGGGA
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880 CAAGT-ACAGCACCTCCA-----GGCTGCTTTCTCTCAGTATAAGAAAGTTGAGCT
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Publication No. US20030027248A1

GENERAL INFORMATION:
APPLICANT: Bejanin, Stephane
APPLICANT: Bejanin, Stephane
APPLICANT: Tanaka, Hiroaki
TILE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.USZ.REG
CURRENT FILING DATE: 2001-08-06
CURRENT APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-3
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2001-06-29
PRIOR PLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR PLICATION NUMBER: US 60/293,574
                                                                                             402 GluProThrProAlaProGluAspAsnGlyCys-
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1278 TCTTGTGGTCTGCGAG 1293
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SOFTWARE: JPatent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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LOCATION: 965..1133
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LOCATION: 1..475
NAME/KEY: CDS
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         TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cancaration: Sets
TITLE OF INVENTION: Sets
FILE OF INVENTION: Sets
FILE OF INVENTION: Sets
CURRENT FILE OF INVENTION: Sets
CURRENT FILENG DATE: 2001-09-18
PRIOR PELICATION NUMBER: US/60/233,617
PRIOR PAPLICATION NUMBER: US/60/234,052
PRIOR PELING DATE: 2000-09-26
PRIOR PAPLICATION NUMBER: US/60/234,923
PRIOR PLING DATE: 2000-09-25
PRIOR PAPLICATION NUMBER: US/60/235,134
PRIOR PLING DATE: 2000-09-25
PRIOR PAPLICATION NUMBER: US/60/235,637
PRIOR PLING DATE: 2000-09-26
PRIOR PAPLICATION NUMBER: US/60/235,637
PRIOR PLING DATE: 2000-09-26
PRIOR PLING DATE: 2000-09-27
PRIOR PLING DATE: 2000-09-27
PRIOR PRIOR PLING DATE: 2000-09-27
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFUMARE: Patentin version 3.0
LENGTH: 1410
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474.50
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36.278
15.988
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Best Local Similarity:
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FILING DATE: 2001-08-06

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Publication No. US20030027161A1
GENERAL INPORMATION:
APPLICANT: Benjanin. Stephane
TITLE OF INVENTION: HITOAKI
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 91.US4.DIV
CURRENT APPLICATION NUMBER: US/09/992,600A
CURRENT FILING DATE: 2001-11-13
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PRICATION NUMBER: PCT/IB01/01715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 AlaValValProLeuAlaLeuGlnAsnGluPro---ThrProAlaPro 407
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                              Conservative:
Mismatches:
                                                                               US-09-763-712A-2 (1-547) x US-09-924-340-57 (1-1133)
          Length:
Matches:
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    3.99e-17
455.00
47.46%
41.53%
15.33%
                         Percent Similarity:
Best Local Similarity:
Query Match:
Alignment Scores:
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         Pred. No.:
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Mismatches:
Indels:
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PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-06-29
PRIOR PELICATION NUMBER: US 60/298,698
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-15
NUMBER: OF SEQ ID NOS: 114
SOFTWARE: JPALENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 455.00
47.46%
41.53%
15.33%
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                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: 476..964
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 965..1133
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: polyA_site
LOCATION: 1118..1133
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Best Local Similarity:
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NAME/KEY: 5'UTR
LOCATION: 1..475
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                                                                                                                                                  SEQ ID NO 57
LENGTH: 1133
                                                                                                                                                                                  TYPE: DNA
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Fri Mar 21 12:50:43 2003

0 ProdlyLeuPro	d Q Q	4332 AAAACCGGCCCAGTCGGTCCTCAGG 334ProGlyProProGlyLysc
374Gly 374 680 ATCTCTGCAGTGGGTCTGAAAGGAGACCGAGGAGCCACCGGAGAAAGGGGCCTTGCAGGC 739 375 ValProGlyMetProGlyProLysGlyProProGlyProProGlyProSerGly 392 :::	oy oy	
/4U CICCCAGGCCCGGCCCCCCAGGTCCTCAGGTCCTCCAGGCTATGGCAAGATGGGT 799 393 AlaValValProLeuAlaLeuGlnAsnGluProThrProAlaPro 407	qa o	4512 GAAAAGGGACATCCTGGTTTAAŤTC 352GlnGlyLeuGlnGlyThrV
RESULT 5 US-09-919-497-6 US-09-919-497-6 Sequence 6, Application US/09919497 Sequence 10 US20020106662A1 GENERAL INFORMATION: APPLICANT: MULTEY, GEOTIFE IN THE OPERATION OF THE OPERATION OPERATION OF THE OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPERATION OPER	d vo d vo	4572 GGTGACCGAGGGCTCCCTGGAACTC 364 ProGlyProArgGlyLeuProGlyI
09/919,497	qa ko d	4692 CCAAAGGGTAACAAAGGCTCTACTC 383 GlyProProGlyPros 11
NUMBER OF SEQ ID NOS: 100 SOFTWARE: PatentIn version 3.0 EQ ID NO 6 LENGTH: 6158 TYPE: DNA	3	
ORGANISM: Homo sapiens FEATURE: NAME/KEY: Uncurre LOCATION: (2434)(2434) OTHER INFORMATION: n = a, c, g or t/u	da Oy	
: Ey: arity:	90 OX	4849 -CAGATGCAGATGATAATATTCTTC 457
US-09-763-712A-2 (1-547) x US-09-919-497-6 (1-6158)  QY 248 GlyProProGlyProArgGlyProArgGlyAspArgGlySerGlnGlyProProGlyPro 267	da da	
268 Thr	δ δ	496 sAlaGlyGlnProAspAsnTrpGly :::    5087 ATCTGGT
	oy do	uilei 
287 GlyGluArgGlyProlleGlyProAlaGlyProProGlyGluArgGlyGly 303	OY Db RESUI	OY 536 ULYS 537 DD 5152 CAAA 5155 RESULT 6 US-09-954-456-762
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r Identifying Anti-Cancer Therapeutic Agents Using C
                                  sGluGlyLeu-----342
::::|||||||
ACAAGGTCTCCCTGGAGCTGCAGGTGGACG 4451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCTGGTGAAGTCATT-----CAG 4793
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TGATTACTCGGATGGAAGAAATATTTGGTTCC 4907
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TGCAACTCAGCCATCCTGACTTCCCAGATGGTGAATA 5026
AGGGACCTGCAGGAAAGCCTGGTCCAGAAGGTCTTCGG 4391
                                                                                                                                                    CITACCIGGICTCAAAGGIGACCCIGGCICCAAGGGI 4511
                                                                                                                                                                                                                               FGCCCTGATTGGTCCTCCAGGAGAACAAGGGGGAAAAA 4571
                                                                                                                                                                                                                                                                                                 YLeuProGlyValProGlyMetProGlyProLys--- 382
| |||||| ||||||::||||||||::
|TCCACCTGGTCCTCCAGGCTTACCAGGTCCTCAAGGC 4691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGACCCGCTGGCCAGAAGGTGACAGTGGTCTTCCA 4751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGAGCATATGAAATTTCCAATGGGTACTCAGACCAAT 4967
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                                                                                                                yPhe----- 351
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; TITI	TITLE OF INVENTION: Sets FILE REFERENCE: 689290-76	QY	343 Pro	ProGly!
CURI	CURRENT APPLICATION NUMBER: US/09/954,456 CURRENT FILING DATE: 2001-09-18	q	4452 CCT	ccreer
; PRIOR	PRIOR APPLICATION NUMBER: US/60/233,617 PRIOR FILING DATE: 2000-09-18	Qy	351	
PRIC	PRIOR APPLICATION NUMBER: US/60/234,052	qq	4512 GAA	GAAAAGG
PRIC	PRIOR APPLICATION NUMBER: US/60/234,923	Οy	352	
PRIOR .	PRIOR APPLICATION NUMBER: US/60/235,134	qa	4572 GGT	GGTGACC
; PRIOR	APPLICATION P	Qy	364 Pro	Pro61yE
PRIOR		qq	4632 CCT	CCTGGTC
PRIOR		Qy	382	
PRIOR		qq	4692 CCA	CCAAAGO
, PRIOR	PRIOR APPLICATION NUMBER: US/60/235,840 PRIOR FILING DATE: 2000-09-27	δÿ	383 Gly	GlyPro
; PRIOR		qa	4752 GGG	GGGCCTC
; SOFT	NUMBER OF SEQ ID NOS: 2276 SOFTWARE: PatentIn version 3.0	Qγ	403 Pro	ProThr
SEO		q	4794 CCT	CCTTTAC
TYL	TYPE: DNA ORGANISM: Homo saniens	Qy	422 sCy	scysTyı
FE	PERTURES: ICOMO SUPELLIS NAME KEVY: misc feature	qa	4825	
; OTF	nemickati miss_reactive; OTHER INFORMATION: n=a,t,g or c	Qy	442 pLy	pLysSer
	20/ 00% 10	qq	:: 4849 -CA	-cagato
Pred. No.:	Scores: 2.4e-16 Length: 6	٥y	457	i
Percent	455.00 Matches: 1 39.81% Conservative: 3	qq	4908 CTC	CTCAATI
Dest Local S Query Match: DB:	at Simitaticy: 50.51% Mismacres: 75  itch: 15.26% Indels: 180  face: 10 Gane: 18	Οy	463 tVa	tValGly
us-09-7	-954-456-762 (1-6158)	qa	4968 CCA	cca-ecc
	(O) TO	Οy	483 sTr	sTrpLeu
2y 4g	248 GlyProProGlyProArgGlyProArgGlyAspArgGlySerGlnGlyProProGlyPro 267 4012 GRACTRCTACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	qa		    TTGGAT
	10010000000000000000000000000000000000	Qy	496 sAl	sAlaGly
`	111.	qa	:: 5087 ATC	ATCTGG1
	GIIGGITTICCIGGAGAICCIGGICCICCIGGGAACITGGCCCTGCAGGTCAAGAIGGI	Qy	516 uIl	uIleTyr
Db 41	269G1yAsnLysG1yG1nLysG1yG1uLysG1yG1uProG1yProProG1yProAla 286 	qq	   5106 -AT	-ATTTA
		Qγ	536 uLys	's 53
67 G	20) GIGGLUALGGIYFLOIDEGIYFIOAIGGLYFIOGLOAGGIYGIUAIGGIYGIYA 303 	qq	5152 CAAA	A 51
	LysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLysPro	RESULT US-09-	RESULT 7 US-09-954-456-782	-782
Db 42	4272 GAGGGAAGACAGAGGTGAAAAGGGGGAAGCAGGTGCAGAAGGTCCTCCTGGA 4331	S	Sequence 782, P Patent No. US20	12, P
0у з	323 333		APPLICANT: YOU	You
Db 43	4332 AAAACCGGCCCAGTCGGTCCTCAGGGACCTGCAGGAAGCCTGGTCCAGAAGGTCTTCGG 4391		TITLE OF INVEN	INVEN
	ProGlyProFrogluGlyLeu		FILE REFERENCE CURRENT APPLIC CURRENT FILING	PLIC
Db 43	4392 GGCATCCCTGGTCCTGTGGGAGAACAAGGTCTCCCTGGAGCTGCAGGCCAAGATGGACCA 4451		PRIOR APPLICAT PRIOR FILING D	ICAT NG D

0y	ო -	51
an n	4452 CCIGGICCIAIGGGACCICCIGGCITACCIGGICICAAAGGIGACCCIGGCICCAAGGGI	4511
QY	351	351
QQ	4512 GAAAAGGGACATCCTGGTTTAATTGGCCTGATTGGTCCTCCAGGAGAACAAGGGGAAAAA	4571
Οy	352GluGlyLeuGlnGlyThrValGlyGluProGlyVal	363
qa	4572 GGTGACCGAGGCTCCCTGGAACTCAAGGATCTCCAGGAGCAAAAGGGGATGGGGGAATT	4631
QY	364 ProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLys	382
gg		4691
δλ	382	382
qa	4692 CCAAAGGGTAACAAAGGCTCTACTGGACCCGCTGGCCAGAAAGGTGACAGTGGTCTTCCA	4751
οχ	383 GlyProProGlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGlu	402
qa	4752 GGGCCTCCTGGGCCTCCAGGTCCACCTGGTGAAGTCATTCAG	4793
δy	403 ProThrPro-AlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAspLy	422
qq	4794 CCTTTACCAATCTTGTCCTCCAAAAAAGA	4824
Qy	422 sCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGluAs	442
qq	4825GAAGACATACTGAAGGCATGCAAG	4848
Οy	442 pLysSerSerHisLeuValPheIleAsnThrArgGluGln	456
qq	4849 -CAGATGCAGATGATATTCTTGATTACTCGGATGGAATGGAAGAAATATTTGGTTCC	4907
δy	457GhnTrplleLysLysGlaMe	463
QQ	4908 CTCAATTCCCTGAAACAAGACATCGAGCATATGAAATTTCCAATGGGTACTCAGACCAAT	4967
ΟY		483
qq	4968 CCA-GCCCGAACTTGTAAAGACCTGCAACTCCAGCCATCCTGACTTCCCAGATGGTGAATA	5026
ΟŅ	483 STrpLeuAspGlyThrSerProAspTyrLysAsnTrpLy	
qq	5027 TIGGATIGATCCTAACCAAGGTIGCTCAGGAGATICCTICAAAGTTTACTGTAATTTCAC	5086
ΟŅ	496 sAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGluAspCysAlaGlyLe ::::	516
qq	rggr	5105
ΟŻ	516 ulleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspValAsnAsnPheIleCysGl	536
qq	5106 -ATTTATCCAGACAAAAATCTGAGGGAGTAAG-AATTTCATCATGGC	5151
QY	536 uLys 537	
qq	5152 CAAA 5155	
RESC US-C Se ; Se ; GE	RESULT 7 US-09-954-456-782 ; Sequence 782, Application US/09954456 ; Patent No. US20020115057A1 ; GENERAL INFORMATION: ; APPLICANT: Young, Paul	
	ing Anti-Cancer Therapeutic	Agents Using C
	FILE REFERENCE: 689290-76 CURRENT APPLICATION NUMBER: US/09/954,456	
۱۰۰۰۰۰	CURREM FILLING DAIE: ZUUI US-10 PRIOR APPLICATION UNMBER: US/60/233,617	

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---GCCCCCCTGGTCCCCCCGGTCAAGATGGTCGCCCCGGACCCCCAGCCCACCTGGT 1835
                     2016 GAACAAGGCCCTGCTGGCTCCCCC---GGATTCCAGGGTCTCCCTGGTCCTGCTGGTCCT 2072
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                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Gene Logic, Inc.
TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFERENCE: 44921-5028-w0
CURRENT APPLICATION NUMBER: US/09/680,107
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/210,054
PRIOR FILING DATE: 2000-10-02
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ORGANISM: Homo sapiens
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Best Local Similarity:
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        PRIOR AFELING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: US/60/234,923

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-25

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR PILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-26

PRIOR FILING DATE: 2000-09-27

SOFTWARE: PATENTIN NUMBER: US/60/235,863

PRIOR FILING DATE: 2000-09-27

SOFTWARE: PATENTIN VUMBER: US/60/235,863

PRIOR FILING DATE: 2000-09-27

SOFTWARE: PATENTIN VUMBER: US/60/235,863

PRIOR FILING DATE: 2000-09-27

SOFTWARE: PATENTIN VUMBER: US/60/235,863

PRIOR FILING DATE: 2000-09-27

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 782

LENGTH: 6728
APPLICATION NUMBER: US/60/234,052
FILING DATE: 2000-09-20
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US-09-954-456-782
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	Qy	267 ProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAla 286
SULT 9 -09-954-456-786 Sequence 786, Application US/09954456 Patent No. US20020115057A1 GENERAL INFORMATION: TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cand	oy Oy	287 GlyGluargGlyProIleGlyProAlaGlyProProGlyGluargGlyGly 303
	QY	311 318 2759 CCAGCTGGTCCAAATGGTCCCCCGGTCCTGCAAGTCGTGGAGTGAGGGCCCCCCT 2818
AFFILEND DATE: 2000-09-18 APPLICATION NUMBER: US/60/234,052 FILING DATE: 2000-09-20 FILING NATH TOWN TOWN TOWN TOWN TOWN TOWN TOWN TOWN	Qy Db	319
	Qy Db	328 SerGlyAspProGlyProProGlyProProGlyLuglyLeuProGlyProGln 346
AFFLICATION NUMBER: US/00/235,037 APPLICATION NUMBER: US/60/235,638 FILING DATE: 2000-09-26 APPLICATION NUMBER: US/60/235,711	QY	347GlyProProGlyPheGln 352
FILING DATE: 2000-09-27 APPLICATION NUMBER: US/60/235,720 FILING DATE: 2000-09-27 ADDITCATION NUMBER: 05/60/235,720	Qy Db	353 GlyLeuGlnGlyThrValGlyGluProGlyValProGlyPro 366
FILE ACTION NOMBER: 2000-09-27 APPLICATION NUMBER: US/60/235,863 FILING DATE: 2000-09-27 OF SEC IN MOS. 2276	Qy Db	367 ArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLysGlyProProGly 386 :::
Version 3.0	Oy Db	387 ProproGlyProserGlyAlaValValProLeuAlaLeuGlnAsnGluPro 403
	Qy	404
6.53e-16 Length: 5416 444.00 Matches: 115 43.40% Conservative: 23 36.16% Mismatches: 79 14.95% Indels: 102	8	2094 4, Application US IS20020142981A1 NRMATION: Horne, Darci T.
712A-2 (1-547) x US-09-954-456-786 (1-5416)  IleArgLeuAspSerValSerLeuArgMetGlnGlnAspLeuMetArgSerArgLeuAsp 216  iii		APPLICANT: VocKLey, Joseph G. APPLICANT: Scherf, Uwe APPLICANT: Gene Logic, Inc. TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO
1000 233		CURRENT FILING DATE: 2001-06-14 CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14 PRIOR FILING DATE: 2000-06-14
		PRIOR FILING DATE: 2000-10-02 NUMBER OF SEQ ID NOS: 3950

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444.00
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SOFTWARE: Patentin Ver.
SEQ ID NO 2094
LENGTH: 5416
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ORGANISM: Homo sapiens
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Sequence 104, Application US/10044090

Sequence 104, Application US/10044090

Patent No. US/20020137081A1

GENERAL INFORMATION:
APPLICAMY: Olga Bandman

TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION

TITLE OF INVENTION UMBER: US/10/044,090

CURRENT APPLICATION NUMBER: US/10/044,090

CURRENT APPLICATION NUMBER: US/10/044,090

SOFTWARE: PERL PROGram

SEQ ID NO: 850

SOFTWARE: PERL PROGram

SEQ ID NO 104
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3059 CAGGGTCTTCTTGGTGCTCCTGGTATTCTGGGTCTCCCTGGCTCGAGAGGTGAACGTGGT 3118
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                                                      310 GlnGlyProLysGlySerArgGlySerProGlyLysProGlyProGlnGlyPro-----
                                   ---ValProLeuAlaLeuGlnAsnGluPro
                                                                                                                       3179 GGGCCCGTGGTCCTCCTGGTGCTGTGGGTAGTCCTGGAGTCAACGGTGCTCCT 3232
                                                                                                       ---ThrProAlaProGluAspAsnGlyCysPro 413
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OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.19
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Conservative:
Mismatches:
Indels:
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LOCATION: 1492-1495, 1663, 1669, 4012, 4055

) OTHER INFORMATION: a, t, c, g, or other

US-10-044-090-104
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TYPE: DNA
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                                                              386 GlyProProGlyProSerGlyAlaVal-----ValProLeuAlaLeuGlnAsnGlu 402
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                          366 ProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLysGlyProPro
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Indels:
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Matches:
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; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3947
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Best Local Similarity:
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US-09-880-107-3947
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2309 GGATTTGCTGGTCCGGCTGGTGCTGCTGGTCAACCGGGTGCTAAAGGAGAAAAGGAGCC 2368
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                                                             ProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAla 286
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Sequence 206, Application US/09925299

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION:

FILE REPERENCE: PA102
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR PELING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
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OTHER INFORMATION: n equals
NAME/KEY: misc_feature
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SEQ ID NO 206
LENGTH: 5145
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Patent No. US20020055627A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies FILE REFERENCE: PA.02
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
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                                                                                                                                 Conservative:
Mismatches:
Indels:
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                                                                                                         Length:
Matches:
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                           or
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NAME/KEY: misc_feature
LOCATION: (5126)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (5143)
                                                           ; OTHER INFORMATION: n equals a,t,g, US-09-925-299-206
                                                                                                     9.63e-16
440.50
49.328
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                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                              Alignment Scores:
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PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                      OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (17)
OTHER INFORMATION: n equals a,t,g,
NAME/KEY: misc_feature
LOCATION: (5126)
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SOFTWARE: PatentIn Ver. 2.0
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LOCATION: (5143)
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                                                                                                                           ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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                                                                           Sequence 22, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGram
SOFTWARE: PELL PROGram
SEQ ID NO 22
LENGTH: 5432
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; OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.13
US-10-044-090-22
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Search completed: March 21, 2003, 12:31:42 Job time : 295.779 secs

GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
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Command line parameters:
-MODEL-frame+ p21.model -DEV-xlp
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-DG-cgn2\_1/USPTO\_spool/US09763712/runat\_14032003\_100950\_18109/app\_query.fasta\_1.1877
-DB-EST -OFWT-fastap -SUFFIX-rst -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT-0
-UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40 cdi -LIST-45
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-OUTEMT-pto -NORM-ext -HEAFSIZE-50 -MINIEN=0 -MAXLEN=200000000
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-NO\_XLEYX -NO\_MARP -LARGEQUERY -NRG\_SCORES=0 -WART -LONGLOG -DEV\_TIMBOUT=120
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em\_gss\_mus:\* em\_gss\_other:\* em\_gss\_pro:\* gb\_gss:\* em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* em\_gss\_fun:\* em\_gss\_mam:\* em\_gss\_rod:\* gb\_est4:\*
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Mus musculus, Similar to scavenger receptor with C-type lectin, clone IMAGE:2811487, mRNA.
BC009162
BC009162.1 GI:14714370
HTC.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosicomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3305) Strausberg, R. Direct Submission

house mouse. Mus musculus

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

LOCUS DEFINITION

RESULT 1 BC009162

ACCESSION

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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                                                                                                                                                                                                                                                                                                                                                                                                                                          WAP-TGF alpha model. 7 months
                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Conter code: BCM-HGSC
Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunnartne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Submitted (05-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                         Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: h Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                                                                                                                                                       Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.
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Location/Qualifiers

1. 3305

/organism="Mus musculus"
/db_xref="taxon:10090"
/map="C57BL/6J"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AspTrpLeuLysGluLysValGlnSerLeuGlnThrLeuAlaAlaAsnAsnSerAlaLeu
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Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Mammary tumor.
old, gross tissue."
/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pCMV-SPORT6"
757 c 760 g 757 t
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                                         AspLeuHisLysAspalaGluAsnArgThrAlaIleLysPheAsnGlnLeuGluGluArg
                     1041 GACTTACACAAGGATACAGAAAATAGAACAGCTGTCAAGTTCAGCCAACTTGAGGAACGC
                                                                                                                                                                                     SerGlnGlyProProGlyProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluPro
                                                                                                                                                                                                                                                                                                                             321 LysProGlyProGlnGlyProSerGlyAspProGlyProProGlyProProGlyLysGlu
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                                                                                                                              ThrLysHisThrAspAspLeuThrSerLeuAsnAsnThrLeuAlaAsnIleArgLeuAsp
                                                                                                                                          SerValSerLeuArgMetGlnGlnAspLeuMetArgSerArgLeuAspThrGluValAla
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ProlleGlyProAlaGlyProProGlyGluArgGlyGlyLySGlySerLySGlySerGln 310
                                  151 IleIleSerAsnIleSerTyrThrAlaHisHisLeuArgThrLeuThrSerAsnLeuAsn 170
                                                                                                                                                                                                                                                                                                                                                 GluValArgThrThrCysThrAspThrLeuThrLysHisThrAspAspLeuThrSerLeu
                                                                                                        AsnAsnThrLeuAlaAsnIleArgLeuAspSerValSerLeuArgMetGlnGlnAspLeu
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/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone_ilb="NHH_MGC_129"
/clone_ilb="NHH_MGC_129"
/lab host="DH10B (phage-resistant)"
/note="Grgan: olfactory ppithelium; Vector:
pCWY-SPORT6.1.ccdb; Site_1: EcoRY; Site_2: Not1; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
                                                                                                                                                                                                                             957 bp mRNA linear EST 21-AUG-2002 ACMCOURT_8763247 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6313500 BQ955927 aquence. BQ955927.1 GI:22371405
                2180
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         GluTrpLysTrpLeuAspGlyThrSerProAspTyrLysAsnTrpLysAlaGlyGlnPro
                                   AspAsnTrpGlyHisGlyHisGlyProGlyGluAspCysAlaGlyLeuIleTyrAlaGly
                                                                     GlnTrpAsnAspPheGlnCysGluAspValAsnAsnPheIleCysGluLysAspArgGlu
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284
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8
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Matches:
Conservative:
Mismatches:
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Location/Qualifiers
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                                                                                                                         GCAGTACCATCATCCATATTA 2321
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1460.50
93.738
89.038
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TITLE
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481
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BQ955927
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BQ891432
AGENCOURT_8754195 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6332754
5', mknA sequence.
BQ891432.1 GI:22283446
EST.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 936)
NIH-MGC http://mgc.nci.nih.gov/.
                                                   847 AGGCTTGCCAGGGTGCCAGGCATGCCCTGGGGCCTAAGGGACCACCTGGGCCCTCCAAG 906
370 oGlyLeuProGlyValProGlyMetPro--GlyProLysGlyProPro-GlyProProGl
                                                                                                                                389 yPro---SerGlyAlaValValProLeuAla---LeuGlnAsnGluPro 403
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667 330 727

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                                                       Freeman
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/db_xref="taxon:10090"
/clone="IMAGE:6332754"
/clone=lib="MIH_MGC_130"
/lab_host="DH10B (phage-resistant)"
/note="Organ: otcoysts: y Vector: pCMy-SPORT6.1.ccdb;
Site_1: EcoRy: Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.95 kb.
constructed by ResGen, Invitrogen Corp. Note: this is
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 ArgPheGlnLeuPheGluThrAspIleValAsnIleIleSerAsnIleSerTyrThrAla 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HisHisLeuArgThrLeuThrSerAsnLeuAsnGluValArgThrThrCysThrAspThr 179
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                                                                          CDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

MAN Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13790 row: n column: 19

Plate: LAM13790 row: n column: 19

High quality sequence start: 25

High quality sequence store: 632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 ThrAspTrpLeuLysGluLysValGlnSerLeuGlnThrLeuAlaAlaAsnAsnSerAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200 AspSerValSerLeuArgMetGlnGlnAspLeuMetArgSerArgLeuAspThrGluVal
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                                                                                                                                                                                                                                                                                                                                                                6 others
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272
16
9
6
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Mismatches:
                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie,
Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
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                          Contact: Robert Strausberg, Ph.D.
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89.77%
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BQ713873 861 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8482828 NIH_MGC_129 Mus musculus CDNA clone IMAGE:6306240
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1 (hases 1 to 861)
1 (hases 1 to 861)
1 (hases 1 to 861)
Nutl-Muc http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Susan L. Sullivan, PhD.

CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blossience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM13721 row: n column: 01
High quality sequence stop: 598.

Location/Qualifiers
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Mus

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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LiAMI1636 row: b column: 17
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 906) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Matches:
Conservative:
Mismatches:
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/clone="IMAGE:5251888"
/clone=lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross ti/dev_stage="7 months"
/lab_host="DH10B"
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B1456109
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BST.
house mouse.
Mus musculus
Rike musculus
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone="INAGE:6330794"
/clone=lib="NIH_MGC_130"
/lab_host=DH10B (phage-resistant)"
/note="Organ: otocysts; Vector: pCWV-SPORT6.1.ccdb; Site=1: EcoRv; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dr. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is
                                                                                                       602
                                                                                                                          CDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

http://image.llnl.gov

High quality sequence stop: 352.
542
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freema Ph.D.
                                                                                                                                                                       346 GlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGly
                                                                                                                                                                                                                                                                 424 yrTyrPheSerVal---GluLysGluIlePheGluAspAlaLysLeuPheCysGluAspL
                                 326 GlyProSerGlyAspProGlyProProGlyProProGlyLysGluGlyLeuProGlyPro
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/organism="Mus musculus"
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Mus musculus
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                                                                                                                                                                     nAspLeuHisLysAspAlaGluAsnArgThrAlaIleLysPheAsnGlnLeuGluGluAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             786 GGATCTCAGGGGACCAACTGGGTCCAACTTGGCAACAAGGGGAACAAAAAAGGGAGAGAA
                                                                                  MetTyrSerHisAsnValValIleMetAsnLeuAsnAsnLeuAsnLeuThrGlnValGln
                                                                                                                       GlnArgAsnLeuIleThrAsnLeuGlnArgSerValAspAspThrSerGlnAlaIleGln
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884
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118
14
9
                 Conservative:
Mismatches:
Indels:
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Length:
Matches:
                                                                US-09-763-712A-2 (1-547) x BQ934501 (1-884)
6.64e-75
1219.50
92.54%
86.44%
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	Oy 484 TrpLeuAspGlyThrSerProAspTyLySaSn 494	Email: cgapbs-r@mail.nih.gov Tissue procurement: ATCC  CDNA Library Preparation: Rubin Laboratory  CDNA Library Preparation:  CDNA Library Preparation:  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  DNA Sequencing by: Agencourt Bioscience Corporation  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  http://image.lln.gov  Plate: LLCM2377 row: c column: 09  High quality sequence stop: 656.  High quality sequence stop: 656.  Coation/Qualifiers  Source // Ocation/Qualifiers  // Ab_xref="Itaxon:966" // Clone="Itaxon:966" // Clone="Itaxon:966" // Lissue_type="epidermoid carcinoma, cell line" // Alab_host="Namary Alab_nost="Distribution" // Alab_host="Distribution" // Alab_host="Distribut	Site_2: ECORI; CDNA made by oligo-dr priming.  Directionally cloned into EcoRIXAnol sites using the following 5' adaptor: GGACGGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."  Alignment Scores:  Pred. No.:  Score:  Score:  Conservative:  Bast Local Similarity:  99.43*  Mismatches:  DB:  Mismatches:  14 Gaps:  Gaps:  Ouery Match:  14 Gaps:
A REG	COMMENT CONTACT: Robert Strausberg, Ph.D.  Email: cgapbs_r@mail.nih.gov     Tissue Procurement: Gilbert Smith, Ph.D.     CDNA Library Preparation: Life Technologies, Inc.     CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)     DNA Sequencing by: Incyte Genomics, Inc.     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:     http://image.llnl.gov     Plate: LLAM9128 row: m column: 13     High quality sequence stop: 580.     FEATURES     I. 580     Concerion Consortium (LOSD)     //rapism="rwbk"     //dranism="wus musculus"     //strain="rwbk"     //db_xref="taxon:10090"     //clone="IRAGE:9962292"     //clone="IRAGE:9962292"     //clone="IRAGE:9962292"     //dev_stage="tumor, blopsy sample"     //dev_stage="tumor, blopsy sample"     //dev_stage="tumor, blopsy sample"     //dav_stage="tumor, blopsy sample"     //dab_bost="DH10B"     //note="Organ: mammary; vector: pcMv-SPORT6: Site 1: SalI:	Site_2: NotI; cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator Providing samples: Gilbert Smith, NIH"  Alignment Scores: Alignment Scores: 1.9e-61 Length: 580 Score: Percent Similarity: 96.34* Mismatches: 7 Best Local Similarity: 92.67* Mismatches: 7 Ouery Match: 124.7 x BE910803 (1-580)  Qy 304 LysGlySerGlnGlyProLysGlySerArgGlySerProGlyLysProGly 323 HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	124 ProGINGIyProSerGlyAspProGIyProProGIyProProGIyLySGLUGIyLeuPro

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AL568743 LIL_FL002_PL1 Homo sapiens cDNA clone CSODE005xH04 3 prime
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ner: Oligo dT
/dev_stage="7 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dr
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIW
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Contact: Robert Strausberg, Ph.D.
Email: capabs=r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Prayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8316 row: k column: 12
High quality sequence stop: 551.
S. Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                          Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
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Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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221 c 217 g 290 t 17
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Matches:
Conservative:
Mismatches:
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916.50
91.15%
90.62%
                       Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 967)
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Query Match:
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ORGANISM
                                                                                                    AUTHORS
TITLE
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COMMENT
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Jest="Botu tot emultyoute a newborn, must in adult islet"

Jev_stage="Embryonic day 10.5, E12.5, E16.5, newborn, adult, mixed"

Jab_host="Delion"

Jab_host="Delion"

Jab_host="Delion"

Jab_host="Wector: pSPORT1; Site_1: Not I; Site_2: Sal I; Five libraries representing E10.5/12.5 pancreas, and adult islets of Langerhans were seperately constructed using Superscript plasmid Library kit (Life Technologies). cDNA was made by oligo-dr priming and size-selected by column fractionation. Libraries were amplified once on Solid support and plasmid DNA from each library was prepared and mixed in equal amounts. The mixed library DNA was normalized by method #4 from Bonaldo, Lennon, and Soares 1996 Genome Research 6:791-806; 0.5 microgram and Soares single-stranded mixed library plasmid DNA was mixed with 5 micrograms PCR product representing mixed library inserts and hybridized to an Ecot of 6. Single-stranded (unhybridized) plasmids were isolated by hydroxyapatite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 581)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T.,
Endocrine Pancreas Consortium
L Onpublished (2000)
Other_ESTS: ii60h06.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Endocrine Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harvard University, Howard Bughes Medical Institute bept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
                                                                                                                                                                                                                                                                                       ii60h06.yl Melton Normalized Mixed Mouse Pancreas 1 N1-MMS1 Mus musculus cDNA clone IMAGE:5946107 5' similar to TR:09UM15 Q9UM15 CSR2.; mRNA sequence.
BQ127513.1 GI:20201424
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   532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fax: 617-495-8557
Email: dmelton@blobp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by
Mashington University Genome Sequencing Center This clone is
available royalty-free through LLNL; please contact the IMAGE
consorttum (Info@lange.llnl.gov) for further information
Seq primer: -40RP from Gibco
High quality sequence stop: 446.
                                    /strain="ICR"
/db_xref="taxon:10090"
/clone="IMAGE:5946107"
N1-MMS1"
N1-MMS1"
516 LeulleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspValAsnAsnPheIleCys
                                                                                                                                                                              GluLysAspArgGluThrValLeuSerSerAlaLeu
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/organism="Mus musculus"
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usa

MD 20850,

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Mus musculus
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Hegde, P., Oi, R., Abernathy, K., Dharap, S., Caspard, R., Gay, C., Holi, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
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  library.
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Contact: John Quackenbush
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used to make this
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177
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chromatography and
159 c 114 g
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AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 638) Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB248064 RIKEN full-length enriched, 7 days neonate cerebellum Musmusculus cDNA clone A730023E20 3', mRNA sequence.
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149
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/db_xref="taxon:9606"
/clone_lib="haGE resequences, MAGE"
/note="Vector: pBluescriptsKm"
112 c 143 g 121 t
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Conservative:
Mismatches:
Indels:
The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 115
Seq primer: Reverse.
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842.00
98.68%
98.03%
28.36%
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Length:
Matches:
Conservative:
Mismatches:
Indels:

3.31e-48 831.00 93.25% 87.12% 27.99%

146 t

146 g

134 c

TITLE JOURNAL COMMENT

DASE COUNT 212 a ORIGIN Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Ouery Match:	US-09-763-712A-2 (1-547)  Qy 385 ProGlyProProGl;  Db 3 CCTGGCCCTCCAGG  Qy 405 ProAlaProGluAsi	63 425 123 145 183	Oy 465 GlyArgGluSerHi.  Db 243 GGGAGAGAAGCCAA  Qy 485 LeuAspGlyThrSe.  Db 303 CTAGACGGTCACC  Qy 505 H16GlyHisGlyPr.  Db 363 AGTGGCCATGGCCA	OY 525 PheGInCysGluds;  Db 423 TTCCAGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	ACCESSION BF805750 VERSION BF805750.1 VERYWORDS EST. Numan. ORGANISM HOMO Saplens ENKATYOLE; MAMMALIA; EUKATYOLE; MAMMALIA; EUKATYOLE I (bases I AUTHORS Dias Neto, E.	Goldman, G.H.  Brunstein, A.,  M.J., Soare  M.J., Soare  Simpson, A.J.  TITLE Shotgun sequence tag  JOURNAL Proc. Natl.,  MEDLINE 20202663  COMMENT Contact: Sim
Okazaki,Y., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki, D., Shibata, K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Muramatau,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatau,M., and Hayashizaki,Y.  RIKEN Mouse ESTS (Arakawa,T., et al. 2001)  On Jul 6, 2000 this sequence version replaced gi:8940810.		1ra 55	. 57 .	çen C		GAGAGAGAGAGAGCCAAAGAGCTCTTTTTTTTTTTTTTT

FEATURES

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511 bp mRNA linear EST 12-JAN-2001 071100-464-c02 CI0173 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "., García Correa,R., Verjovski-Almeida,S., Briones,M.R., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., .., Carvalho,A.F., Matsukuma,A., Baia,C.S., Simpson,D.H., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare es,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is
Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Uutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      uencing of the human transcriptome with ORF expressed
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of Cancer Genetics
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/organism="Homo sapiens"

/db_rafe" "Lavon: 9606"

/clone_lib="C10173"

/dev_stage="Adult"

/dev_stage="Adult"

/note="Organ: colon_ins; Vector: puc18; Site_l: SmaI;

Site_2: SmaI; A min1-library was made by cloning products

derived from ORESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)

profiles into the pUC 18 vector. Reverse transcription of

tissue mRNA and cDNA amplification were performed under

low stringency conditions."
                                                            Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QVI&t2=QVI-CI0173-
071100-464-c02&t3=2000-11-07&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 492.
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364
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Fax: +55-11-2707001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 808)

NIH-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

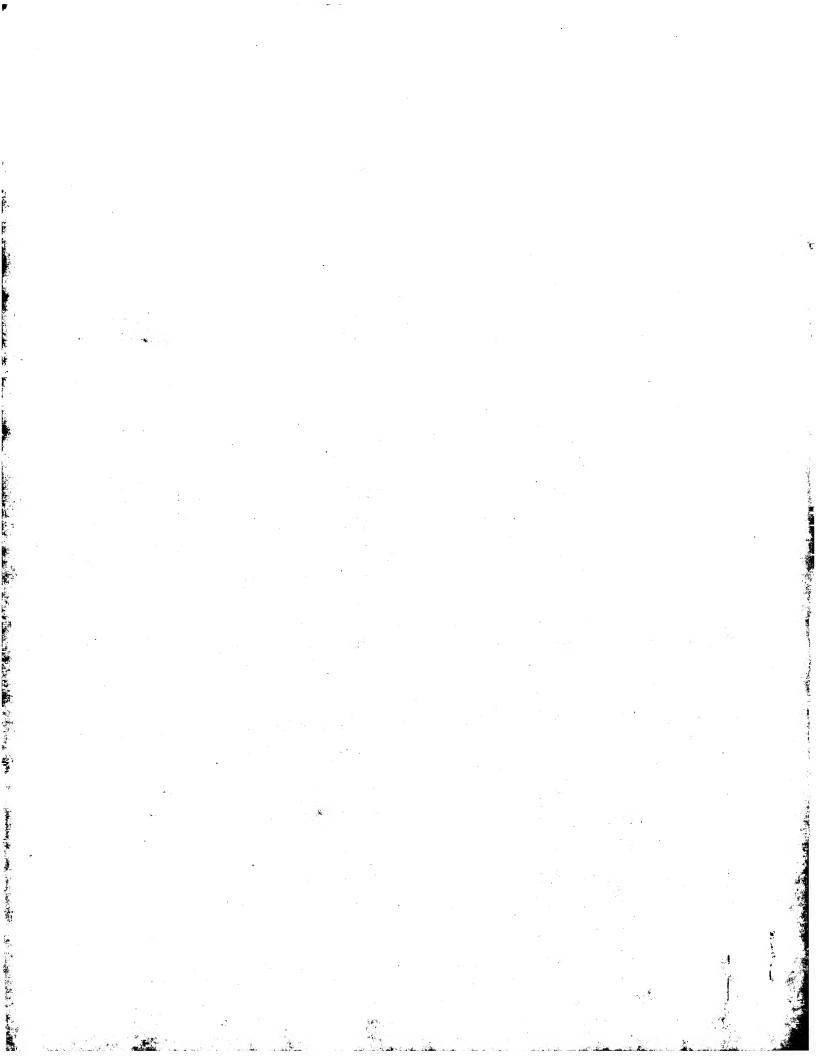
Lonpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, Gov
Tissue Procurement: Dr. Jim Lin, W. Bento Soares, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found the I.M.A.G.E. Consortium/LINL at:

http://mage.linl.gov
This clone was contributed by the Brain Molecular Anatomy Project
BQ771366 808 bp mRNA linear EST 26-JUL-2002
UI-M-FIO-byu-g-09-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
IMAGE:5702432 5', mRNA sequence.
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/organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:5702432"
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                                               BQ771366
BQ771366.1 GI:21979842
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AC024368 Homo sapi
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-D=GenEmbl. OFMT=fastap -SUFFIX=rege -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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Listing first 45 summaries
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Ohtani, K.
Direct Submission
Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College,
Department of Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa,
Hokkaido 078-8510, Japan (E-mail:Ohtani@esahikawa-med.ac.]p,
Tel:+81-166-68-2393, Fax:+81-166-68-2399)
         PRI 21-NOV-2001 complete cds.
                                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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J. Biol. Chem. 276 (47), 44222-44228 (2001)
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Mammalia; Eutheria; Primates;
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; Euteleostomi;  e, Homo.  Qy 201 AlaProGluAspAsnGlyCysProProHiSTrpLysAsnPheThrAspLysCysTyTTyr	Db 1138 Qy 241 Db 1198 Qy 261 Db 1258	Qy 281 ASPGIYTH/SerProASPTY/LIYSASATTPLYSAAAGLYGINProASPASTTPGIYHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	321 1438 341 1498	RESULT 3   AX490920	40 ACCESSION 40 VERSION KEYWORDS 597 SOURCE	60 ORGANISM 657 REFERENCE	PTO 80 AUTHORS 111 CCT 717	100	120 FEATURES Location/Qualifiers 1. 2005 Source 1. 2005 /organism="Homo sapiens" 837 /db_xref="taxon:9606"	Pro 140 BASE COUNT 606 a 493 C 491 g 415 t ORIGIN CT 897 Alignment Scores:	Classical Content of the content o	Query Match: DB: DB: US-09-763-712A-2_COPY_20	Pro 200   Qy 1 MetGlnGlnAspLeuMetA:
<pre>1 Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata Mammalla; Eutherla; Primates; Catarrhini; Hominida 1 Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters, and Ye., W.</pre>	Q Q Q Q Q X X X X X	1. (US) Location/Qualifiers 1. 2005 /organism="Homo sapiens" /db_xref="taxon:9606"  T 606 a 493 c 491 g 415 t	-58 Length: 00 Matches: & Conservati % Mismatches % Indels: Gaps:	US-US-/1ZA-ZCOFY_ZUB_S47 (1-342) x AX454442 (1-2005)  QY	MetGluGluMetLysLeuValaspSerLysHisGlyGlnLeuIleLysasnPheThrIle 	LeuGlnGlyProProGlyProArgGlyProArgGlyAspArgGlySerGlnGlyProPro	. GlyProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProProGly 	AlaGlyGluArgGlyProIleGlyProAlaGlyProProGlyGluArgGlyGlyLysGly	SerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLysProGlyProGln	GlyProSerGlyAspProGlyProProGlyProProGlyLySGluGlyLeuProGly  	GINGIyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProfit	ProArgGlyLeuProGlyLeuProGlyWalProGlyMetProGlyProLysGlyProPro	. GlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThr
ORGANISM REFERENCE AUTHORS	TITLE JOURNAL	FEATURES source BASE COUNT	Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Query Match: DB:	05-09-763 Qy 1 Db 478	Qy 21 Db 538	Qy 41 Db 598	Qy 61 Db 658	Qy 81 Db 718	Qy 101 Db 778	Qy 121 Db 838	Qy 141 Db 898	Qy 161 Db 958	Qy 181

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
I (bases I to 2641)
Bandman,O., Hillman,J.L., Tang,Y.T., Lal,P., Yue,H., Baugh
Lu,D.A. and Azimzai,Y.
Extracellular matrix and adhesion-associated proteins
Patent: WO 0068380-A 39 16-NOV-2000;
Incyte Genomics, Inc. (US)
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AB038518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nakamura, K., Funakoshi, H., Miyamoto, K., Tokunaga, F. and Nakamura, T. Molecular cloning and functional characterization of a human scavenger receptor with C-type lectin (SRCL), a novel member of a scavenger receptor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical School, Division of Biochemistry, Biomedical Research Center; 2-2 yamadaoka, Suita, Osaka 565-0871, Japan (E-mail:knakamur@onbich.med.osaka-u.ac.jp, Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="BAB39147.1"
/db_xref="GI:13365515"
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                                 PheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGluAspLysSerSer
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/db_xref="taxon:9606"
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This clone (DKFzp547G1215) is available at the RZPD in Berlin.
This clone (DKFzp547G1215) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1886 bp mRNA linear PRI 20-MAR-2002 DKFZp547G1215 (from clone DKFZp547G1215).
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/tb_xref="stion-"AIKFNQLEERFQLFETDIVNIISNISYTAHHLRTLTSNLNEVRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EUKATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (basea; 1 to 1886)

Koehrar,K., Beyer,A., Mewes,H.W., Weil,B. and Wiemann,S.

Direct Submission

Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152

Martinsried, GERWANY

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKF2); Email s.wiemann@dkfz-heidelbergoide; sequenced by BMFZ (Biomedical Research Center at the Charite, Perinformany) within the CDNA sequencing consortium of the Germann Canner Conter (DKF2); Emilia (DKF2) (Conter at the Charite, Dermin Conter at the Charite, Dermin Conter (DKF2)) (Conter at the Charite, Dermin Conter at the Charite, Dermin Conter at the Charite, Dermin Conter (DKF2) (Conter at the Charite, Dermin Conter at the Charite, Dermin Conter (DKF2) (Conter at the Charite) (Conter at the Charite)
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                                                                                                                                                                                                                                                                                                                                   /clone="bkFzp547G1215"
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//clone_lib="547 (synonym: hfbr1). Vector pSport1; host
DH10B; site="Not1 + Sal1"
2069 TITICAGITGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA 2128
                                        260
                                                                                                               280
                                                                                                                                                                                      281 AspGlyThrSerProAspTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHis 300
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                                                                                                             261 ArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeu
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KANNDTLEDMNSQLSSFTGQMNNTTTISQANGQSLKDLQDLKKDTBNRTAVNELNT
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KGDRGSQGPPGPTGKKGQKGEKGEPGPPGAGERGTIGPVGPPGERGSKGSKGSQGPK
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KEIFEDAKLFCEDKSSHLVFINSREEQQWIKKHTVGRESHWIGLTDSEQESEWWWLDG
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Ohtani, K., Suzuki, Y., Eda, S., Kawai, T., Kase, T., Keshi, H.,
Sakat, Y., Fukuoh, A., Sakamoto, T. and Wakamiya, N.
Direct Submission
Submitted (18-JAN-2002) Katsuki Ohtani, Asahikawa Medical College,
Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa, Hokkaido
078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:81-166-68-2393, Fax:81-166-68-2399)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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AspClyThrSerProAspTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHis
                                                                                                                         GATGGGACATCTCCCAGACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCAT
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                                             ArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeu
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SPVDYKNWKAGQPDNWGSGHGPGEDCAGLIYAGQWNDFQCDEINNFICEKEREAVPSS
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Oy Db 2	301 GlyHisGlyProGlyGluAspCysAlaGlyLeuIleTyrAlaGlyGlnTrpAsnAsPPhe 320 	Perc Best Ques DB:	Percent Similari Best Local Simil Query Match: DB:
Οy	321 GlnCysGluAspValAsnAsnAsnPheIleCysGluLysAspArgGluThrValLeuSerSer 340	)-Sn	US-09-763-712A-2
Dp 5	2252 CAGTGTGATGAAATCAATAACTTCATTTGTGAGAAAGGGAGGCAGGC	Qy	1 MetGln
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Dp 3	2312 ATATTA 2317	Qy	21 MetGlu
RESULT 8	. 8 19	qu	1337 ATGGAA
LOCUS	AB038519 Mus muscu	λō .	
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REFERENCE AUTHORS		ΩD	1517 GCGGGT
TITLE	Molecular cloning of a mouse scavenger receptor with C-type lectin (SRC)(1), a novel member of the scavenger receptor family	δδ.	
MEDLINE		<u>a</u>	15// TCCAAA
REFERENCE AUTHORS		Qy	
TITLE	Direct Submission AL Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medica	QC .	1637 GGACCT
	School, Division of Biochemistry, Biomedical Research Center; 2-2 yamadaoka, Suita, Osaka 565-0871, Japan	δλ	141 GlnGly
	(E-mail:knakamur@onbich.med.osaka.u.āc.jp, Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)	qa	1697 CAGGG
FEATURES	5	δλ	161 ProArg
2		qa	1757 CCTCGG
б	gene 1.3291	QY	181 GlyPro
S	/gene="srcl" 772305	qa	1817 GGCCCT
	/gene="srcl" /codon_start=1	λō	201 AlaPro
	<pre>/product="scavenger receptor with C-type lectin" /protein_id="BABB2497.1"</pre>	qa	
	/db_xref="G1:18146952" /translation="MKDDFAEREVOSFGYKRFGTHEGTOCTKCTNNWALKFSTVLLY	è	221 Pheser
	ILCALLTITVAILGYKVVEKMDNVSDGMETSHQTYDNKLTAVESDLKKLGDQAGKKAL STNRFI STRPRSDIILDIROOLOFTTREFTSKNOTTIFFI DAGDELYDDOGGI KFIT ONN	5 E	
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	KGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGTIGPVGPPGERGSKGSKGSQGPK GSRGSPGKPGPQGPSGDPGPPGFRGGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPG	ον	261 ArgGlu 
	LPGVPGMPGPRGPPGPPGPSGAMEPLALQNEPTPASEVNGCPPHWKNFTDKCYYFSLE KETLEDAKLPCEDKSSHLVPINSREEOOWIKKHTVGRESHWIGLTDSEOESEWKWLDG	qa	2057 AGAGAA
,	SPVDYKNWKAGQPDNWGSGHGPGEDCAGLIYAGQWNDFQCDEINNFICEKEREAVPSS IL"	Oy	281 AspGly
ď	polyA_signal 32463251 /dene="s*r]"	qa	2117 GACGGG
BASE CO	COUNT 1013 a 757 c 759 g 762 t	Qy	301 GlyHis
Aliqum		qa	2177 GGCCAT
Pred.	Pred. No.: 1.74e-53 Length: 3291	02	321 GlnCys

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Homo sapiens SRCL mRNA for scavenger receptor with C-type lectin
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KANDTLEDNNSQLNSFTGQMENITTISQANGDNLKDLQDLHKDAENRTAIRFNQLEE

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LPGVPGMPGPKGPPGPPGSGAPPTANNPLALONEPTPAPEDNSKSKPSLQPGGGGSACA"

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Nakamura,K. Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura,T.
Molecular cloning and functional characterization of a human
scavenger receptor with C-type lectin (SRCL), a novel member of a
scavenger receptor family
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Submitsed (04-DEC-2000) Kenji Nakamura, Osaka University Graduate
School of Medicine, Division of Biochemistry, Biomedical Research
Center; 2-2 yamadaoka, sulta, Osaka 565-0871, Japan
(E-mill:knakamur@onblch.med.osaka-u.ac.jp, Tel:81-6-6879-3783,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1 MetGlnGlnAspLeuMetArgSerArgLeuAspThrGluValAlaAsnLeuSerValIle
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Location/Qualifiers
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AUTHORS
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205	2523 ATTTTTATTTTCCTTTTTGTAGAACAGGGTCTTGCTATGTTGCCCAGGCTGGTCTTGA 205	QY         205           Db         2763           GTTTTACATCCTCACTCTGGAGATAGATGGGCTCCCTCGGTTAGCTCCATCAACATGTGG         2822           QY         205           Db         2823           ATGGAACCTCTGCTATTGATGATAATTTCTTTTTGAGAAAGGTGTTAGATG         2882           QY         205           Db         2883           TACGGTGCTTTTGATAATTAAAACCTTTGGCAAAACTCGAATGTTTGGTAG           2883         TACGGTGCTTCTAGTCTTTTGATAATTAAAACCTTTGGCAAAACTCGAATGTTTGGTAG           2883         TACGGTGCTTCTAGTCTTTTGATAATTAAAACCTTTTGGCAAAACTCGAATGTTTGGTAG           2883         TACGGTGCTTCTAGTTAAAAACCTTTTGGCAAAACTCGAATGTTTGGTAG		

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6: gap of unknown length
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7: gap of unknown length
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7: contig of 10054 bp in length
7: contig of 12523 bp in length
7: gap of unknown length
8: contig of 13788 bp in length
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/db_xref="Laxon:10116"
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NOTE: This is a "working draft' sequence. It currently consists of 28 contigs. The true order of the pieces is not known and their order in this sequence record is
Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Tayloro, T., Tayloro, T., Tayloro, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Wullliamson, A., Wleczyk, R., Wooden, S., Worley, K., Wu, Y. E., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission Submission Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:2030333.
                                                                                                                                                                                                                                                                                                                                                                               Department
                                                                                                                                                                                                                                                                                                                                                                      Submitted (21-FEB-2002) Human Genome Sequencing Center, Departmer of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 130763)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    as soon as it is available and the accession number will be preserved
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Assembly program: Phrap; version 0.990329
Consensus quality: 113686 bases at least Q40
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Consensus quality: 117044 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
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contig of 1865 by
gap of unknown ly
contig of 1587 bl
gap of unknown ly
contig of 1911 by
gap of unknown ly
contig of 1505 by
gap of unknown ly
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gap of unknown l
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gap of unknown
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gap of unknown
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----- Summary Statistics
Sequencing vector: Plasmid;
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23698:
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Direct Submission
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δý	158	ValProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLys 177	
do .	14	GTACCTGGACCTCGGGGGCTACCAGGCTTACCAGGGGTGCCAGGCATGCCTGGGCCCAAG	268
da da	14207	GlyProFigEroProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGlu	15287
Qy Db	198	Prothrproalaprogluaspasn	Oy 288 LysAsnTrpLysAlaGlyGlnPT
٥y	205		308
QO	14327	GCAGTGTAGGCTTGGCTAAACCAGACCTCAGGAGTCCCCTAATTACACTTAATATCAG 14386	Db 15371 ATATGTGAATTGTCATGCTTCTT
Qy	205	502	r 11 677
qq	14387	GGACCCTATGTGTTCCTCTGGATGCCTCGGTGCTGTCACTCAGGACCCTGTGTTCCTGCT 14446	LOCUS AC114677 DEFINITION MUS musculus clone RE
Qγ	205	205	NO
QΩ	14447	TAAACATTATCAGGACTCTACTCATTTAGATGAGCCAGGGCCCTCAGAAGATACCTATACC 14506	N NS
Qy	205	205	SOURCE house mouse. ORGANISM Mus musculus
Q	14507	CCAAGTACTTATTTCAAGCTATCCTGCACCGGCTGCTCCTGACCATCCTTCCT	Mam Mam
Οy	205	502	REFERENCE 1 (bases 1 to 182029 AUTHORS Birren, B., Linton, L.,
qq	14567	TCTTCTTTCTCCTAGAAACAGACCATTCCATCAATTAACTCCATCAGTATGCAGAFGGGG 14626	
Qy	205	505	REFERENCE 2 (bases 1 to 182029 AUTHORS Birren, B., Linton, L.,
qa	14627	TTTCTGTGATAGACCACACTCTGGTTTTGCTTAAGAAGCTGCTGTGGTGTCTCTTTTT 14686	Anderson, S., Barna, N. Boukhgalter, B., Brown
0γ	205	505	Chazaro, B., Choepel, Y Cook, A., Cooke, P., De
qa	14687	GACCATTAAGTCTTCACAAAACTCTGTTCTAGTTAGGAAACAAGCCATGTGGGGTCACTCA 14746	Ginde, S., Gord, S., Go
Qγ	205	502	Kamat, A., Karatas, A.,
Q	14747	TGCTGGTCCATGAACTTTGGTTCTGAAGTACACTTGTTTACAAGCTCCAGCTGATCCAAG 14806	Landers, T., Lenoczky, MacLean, C., MacGonaló
٥y	205	502	Mihova, T., Mlenga, V.,
QΩ	14807	ACTGACAATGAGTATCAGGGCCCACCCACTTTCTTCTTTCT	NOIDU, C., NOFMEN, C.H. Oliver, J., Peterson, K
Qγ	205	502	Roman, J., Rosetti, M.,
qq	14867	CCAACCCAATCACAGCCTTTCCACACTGTGTGTGTTTCACTATTGTGTACTGTAAAATCC 14926	Scaman, S., Severy, P., Strauss, N., Subramani
Qγ	205	502	Topham, K., Travers, M. Viel, R., Vo, A., Wilso
qq	14927	ACAACTGTGAACATCTGTCCATGTTCTGTACAGGACACTCCATTGGCATGCAAGCAGTG 14986	TITLE Direct Submission
0γ	205	502	
QΩ	14987	TGAGGCTGTCACTTTGGTATCTTAAACATAGCTGAGGAAATGCAGAGTGCCTTTTTTTT	REFERENCE 3 (bases I to 182029 AUTHORS Birren, B., Linton, L.,
ΟŊ	206		Anderson, S., Barna, N. Boukhgalter, B., Brown Chazaro, B., Choepel, Y.
q	15047	. AGATCAACATTTAAAAACGTTACATTCCTAGGATGTCCGCCTCACTGGAAGAACTTCACA 15106	
Oy Db	216	AsplysCysTyrTyrPheSerValCluLysGluIlePheGluAspAlaLysLeuPheCys 235 	Galagan, J., Gardyna, S Grand-Pierre, N., Hago Johnson, R., Jones, C.,
Qy Pb	236.	GluaspLysSerSerHisLeuValPheIleAsnThrargGluGluGln 251 	Lamazares,R., Landers Liu,G., MacLean,C., Matthews,C., McCarthy Matthews,C., McCarthy Maneus I. , Mihova,T.
٥y		GlnTrp11eLysLysGlnMetValGlyArgGluSerHisTrp11eGly 267	
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Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Sebergy, P., Spencer, B., Stange-Thomann, N., Strojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, R., Travers, M., Travis, N., Trigilio, J., Yassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Vonng, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                  Submitted (10-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Jun 10, 2002 this sequence version replaced 91:21328559.
Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * consists of 10 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1952 1051: gap of 100 bp

* 1052 3806: contig of 2755 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 8.0 in Q20 bases; agarose-fp
Quality coverage: 8.0 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: 213_K19

Center clone name: 213_K19

Sequencing vector: Plasmid; n/s: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 179506 bases at least Q40
Consensus quality: 180723 bases at least Q30
Consensus quality: 180703 bases at least Q30
Insert size: 180000; agarose-fp
Insert size: 181129; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                         All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of reads
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L24628
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128411 182029: contig of 53619 bp in length.
Location/Qualifiers
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8709: contig of 4803 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www-seq.wi.mit.edu
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/db_xref="taxon:10090"
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8810 17263: conti
17264 17363: gap of
17364 36938: conti
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46407 AGCAAAGGATCCAAAGGCTCACAGGGTCCCAAAGGATCTCGTGGGTCCCCAGGGAAGCCT 46466
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46827 AAAACAGCAGGGACCCTGTGTATCCCTCTGGATGCTTCAGTGCTGTCACTCAGGACCCTG 46886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46707 CCAACCCCAGCATCAGAGGTCAACGGTAAGTCCAAATCGTCCTTCTCAGCTAGAATTGTG 46766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLysPro 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGly 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ValProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLys 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyProProGlyProProGlyProSerGlyAlaValProLeuAlaLeuGlnAsnGlu 197
                                                                                                                                                                                                                                                                                                                                                                                   38 PheThrIleLeuGlnGlyProProGlyProArgGlyProArgGlyAspArgGlySerGln 57
                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyProProGlyProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyPro 77
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                                                                                                                                                                                                        901 others
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                                                                                                                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                  69673. .89021 '-
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89122. .128310
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128411. .182029
/note="assembly_fragment"
5 a 37484 c 36555 g 52844 t
                                                /note-"assembly_fragment"
37039. 53226
/note-"assembly_fragment"
53327. 69572
/note-"assembly_fragment"
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Matches:
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           8810. .17263
/note="assembly_fragment"
17364. .36938
/note="assembly_fragment"
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981.00
41.25%
38.21%
50.57%
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		SOURCE		RE		REFERENCE AUTHORS	26		98		46		90		99				86 AUTHORS		45	r.		65		23	TITLE	COMMENT	92		52
TUTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	CCTGTACCCCAAATACTTCTTCAAGATATTCTACACTGGCTGCTCCCT  CCTCATCATCTTCTTCTTCTTCTTAGAAACAGACCATTTTATCAGTTAACT  GCAGATAGGGTTTCTGTGACAGAGTCCACATTCTGGTTTTAGAAACT  GCCTTTCTTCTTTTTGACAGAAAGTCTTTTGCAAAACTATAGTTAG  TGCTGTAAAAGCCTAGCCGACAGTCTTTTGCAAAACTATAGTTAG  TGCTGTAAAAGCCTAGCCAGCAGTCTTTTTGCAAAACTATTACTAGTTAG  TGCTGTAAAAGCCTAGCCAGCCAGTCCACACTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	203	GACCATCCT 47006	203	CCACCAGTA 47066	203	CTGTTGTGG 47126	203	GAGCCAAGC 47186	203	CTTATTTAC 47246	203	TTTTTCTGT 47306	203	TCACTGCTG 47366	203	CACCCATIG 47426	203	AAATGCAGG 47486	CysProPro 209	rereceer 4754			Thrargglu 249 :::       TCAAGAGAA 47665	GlyArgGlu 262	TAGAGATA- 47723			HisGlyHis 302      CATAAACAA 47792	AspPheGln 321	GAATTCAAA 47852
TUTTTAAATCAAGATATTTTAAAAAAAAAAAAAAAAAAAA	CCCTGTACCCCAAATACTTCCTTCAAGATATTCTACA CCTCTACACCCCAAATACTTCCTTAGAAACAGACCATT GCAGATAGGGTTCTTTGTCACAGAGGTCCACATTCTGGT GCCTTTCTCTCTTTGACAGAAGGTCCTTTGCAAAA GCCTTTCTCTCTCTTTGACAGAAGGTCTTTTGCAAAA TGCTTCTCTCTCTTTGACAGAAGGTCTTTTGAAAA CCTCCAGCCCGATCCAGCCCACTCTTGCAAAA GCTTCTCTCTTTTTTAAATCAACAGTTTTTTAAAACTTTT GTGCTGTACAGTCCACACTCTGAGAACTTTTTTTAAATCAACAGTTTTTTTAAATCAACAGTTTTTTTT		CTGGCTGCTCCCT		TTATCAGTTAACT	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	TTTGCTTAAGAAG		CTATACTAGTTAG		GTTCTGAAGTGTG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CACCCCACTTTCT		CACTGTGTGTGT		TTCTACACAGGGA	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AACACAGCTGAGG	AspAsnGly	ACATTCCTA-GGA	rValGluLysGlu  :::	ATTGGAAAAAAAA	uValPheileAsn 	sLysGlnMetVal	GAAAACTATAATT	nGluTrpLysTrp	HORORICARA	OASPASNTrpGly :::::    -AATTCATGGTCT	yGlnTrpAsn	AGAGTATATGAAT
TTTTGACAGAGA TCTTTCCCTTA TCTGTGACAGAGA TCCCAAGCCGACA TCCCAAGCCGACA TCCCAAGCCGACA TTTTAAATCAAC TTTTTAAATCAAC TTTTTAAATCAACACAC TTTTTAAAACACACAC	CCCTGTACCCCAAATACTTCCTTC  CTTCATCTTTCTTTTTCTCTCTTA  GCAGATAGGGTTTCTTTTTTCTCCAAA  GCCTTTCTGTCTCTTTGACAAA  GCCTTTCTGTCTTTTTTAAATCAA  GTGTGTACAGTCCAAGCTAA  GTGTGTACAGTCCAAGCTAAA  GTGTGTACAGTCAACTCAAGCTAAA  GTGTGTACAAGTCAACTCTGAAA  GTGTGTACAAGTCAACTCTGAAA  GTGTGTACAAGTCAACTCTGAAA  GTGTGTACAAGTCTTTTTAAATCAAA  GTGTGAAAGTTCTGTGAAATTCTGTGAAAAT  SPAIALYSLEUPHACYSGIUASPL  11	,	AAGATATTCTACA		SAAACAGACCATT		rccacattctggt		STCTTTTGCAAAA		AAGCCAGACTTTG		STGTATCAGAACC		rcccaccttrctt		ACATCTGCCCGGG		CTTTGATATCTTA		CAGTTAAAACTTT	/STyrTyrPheSe 	SCIACIALITIC	/sSerSerHisLe 	TrpIleLy	ACACTTGGTTGGA	erGluArgGluAs	i i galgalgalah	/sAlaGlyGlnPr	eulleTyrAlaGl	TTTCCAGGTATG
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98120 AGCAAAGGATCCAAAGGCTCACAGGGTCCCAAAGGATCTCGTGGGTCCCCAGGGAAGCT 98179
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                    arbitrary, Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
Assembly program: Phrap; version 0.960731
Consensus quality: 190144 bases at least 040
Consensus quality: 191397 bases at least 030
Consensus quality: 191862 bases at least 020
Insert size: 198000; agarose-fp
Insert size: 19208; sum-of-contigs
Quality coverage: 8.8 in 020 bases; sum-of-contigs
Quality coverage: 9.1 in 020 bases; sum-of-contigs
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188547 193208: contig of 4662 bp in length.
Location/Qualifiers
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1314 3101: contig of 1788 bp in length
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88885. .107450

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107551. .127842

/note="assembly_fragment"
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/note="assembly_fragment
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97

77

57

(1-193208)

214 17 35 297

Conservative: Mismatches: Indels:

Matches:

98839

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TITLE JOURNAL	COMMENT												FEATURES	misc_featu misc_featu misc_featu
	203 GCTG 99079 ,	203	CATTG 99139	203	3CAGG 99199	coPro 209         GCCT 99258	neGlu 229         TGAA 99318	rgGlu 249          agaa 99378	rgGlu 262    	spGly 282 99484	LyHis 302 AACAA 99505	neGln 321   :::  CAAA 99565	HTG 09-SEP-2000 WORKING DRAFT Euteleostomi;	Anderson, M., Inhgalter, B., Tre, A., L., Doyle, M., D., Horton, L., A., Klein, J., Irim, J.,
AGACTTTGGTTCTGAAGTGTGCTTAI	CTTTCTTCACTGTGTGTGTTCACT		rGCCCGGGTTCTACACAGGGACACCC		ATATCTTAAACACAGCTGAGGAAATG	AspasnGlyCysProPro	YyrPheSerValGluLysGluIlePF               ATTTTCAFTGGAAAAAGAATTTT	SerHisLeuvalPhelleAsnThrAi 	-TrplleLysLysGlnMetValGlyArgGlu    :::::    :::::     TTGGTTGGAGAAACTATAAATTTAGAGATA-	rgGluAsnGluTrpLysTrpLeuAs 	31yGlnProaspasnTrpGlyHisGlyHis :::::        AATTCATGGTCTCATAAACAA	yralaGlyGlnTrpAsnAspP   :::   :::   AGGTATGAGTATATGAATGAAT	near ap 18, brata; inidae;	Jione KFII 32462  "C., Lander, E., Allen, N.,  Iy, R., Boguslavkiy, L., Boulo, M., Collins, S., Collymor, K., Domelan, Trest, C., Funke, R., Gage, T.,  G., Hagos, B., Heaford, A.,  G., Kann, L., Karatas, A.,  Macdonald, P., Marquis, M., McLaughlin, J., Melis,
GTGTGGGTCCCTCATGCTGGTCCACAAGCCAGACTTTGGTTCTGAAGTGTGCTTATTAC	CGTCATAAAGCCTAGCCCAACCCAGTCCCACCTTTCTTCACTGTGTGTG		TGTGCTGTACAGTCCACATCTGAGAACATCTGCCCGGGTTCTACACAGGGACACCCATTG		GCATGCAAGTGGTACAAGGCTGTGACTTTGATATCTTAAACACAGCTGAGGAAATGCAGG	GTTCCTTCTGTGTTTTTAAATCAACAGTTAAAACTTTACATTCCTA - GGATGTCCGCCT	HistrpLysasnPheThraspLysCysTyrTyrPheSerValGluLysGluIlePheGlu 	AspalaLysLeuPheCysGluAspLysSerSerHisLeuValPheIleAsnThrArgGlu 	GluGlnGln	SerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGly      -	Thr Ser ProAspTyr LysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHis ::::::        AATTCATGGTCTCATAAACAA	303 GlyProGlyGluAspCysalaGlyLeuIleTyrAlaGlyGlnTrpAsnAspPheGln	ACO16128 HOMO Sapiens chromosome 18 clone RP11-32462 m SEQUENCE, 8 unordered pieces. ACO16128. ACO16128.4 GI:10046526 HTG; HTGS_PHASE1; HTGS_DRAFT. HOMO Sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertel Mammalia; Butheria; Primates; Catarrhini; Hom Eiren, B., Linton, L., Nusbaum, C. and Lander, Eliren, B., Linton, L., Nusbaum, C. and Lander,	Unpublished  2 (bases 1 to 16908)  2 (bases 1 to 16908)  2 (bases 1 to 16908)  2 Inten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barnan, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. G., Johnson, R., Jones, C., Kan, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McEwan, P., McEwan, P., McEwan, J., McEwan, P., McEwan, P., McEwan, J., McKernan, K., McLaughlin, J., Meldrim, J.,
98900 203 98960	Oy 203 -	Qy 203 -	DB 99080 TC	оу 203	Db 99140 G	Oy 204	Qy 210 H:     Db 99259 C	Oy 230 As 1 Db 99319 G	Qy 250 G. L Db 99379 G	Oy 263 St       Db 99437 AC	Qy 283 Tl Db 99485 -	Qy 303 G. Db 99506 AC	RESULT 13 AC016128/C LOCUS DEFINITION ACCESSION VERYWORDS SOURCE ORGANISM REFERENCE	JOHNE JOHNE REFERENCE AUTHORS

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Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M. Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M. Gody,M. Submitted (20-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Sep 9, 2000 this sequence version replaced gi:6649269.
All repeats were identified using RepeatMasker:
Snit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                            ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: 324_G_2

Center clone name: 324_G_2

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 167522 bases at least Q40
Consensus quality: 167248 bases at least Q30
Consensus quality: 167996 bases at least Q30
Insert size: 177000; agarose-fp
Insert size: 168388; sum-of-contigs
Quality coverage: 6.2 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17944 18043: gap of 100 bp 18044 22424: contig of 4381 bp in length 22425 22524: gap of 100 bp 22525 38094: contig of 15570 bp in length 38095 38194: gap of 100 bp 18095 38195 49220: contig of 11026 bp in length 49221 49320: gap of 100 bp 49321 66394: contig of 17074 bp in length 66395 66494: gap of 100 bp 66395 66494: gap of 100 bp 66395 66495 3732: contig of 25198 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91693 91792: gap of 100 bp
91793 120869: contig of 29077 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
11. 17943
/note="assembly_fragment
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120970 169088: contig of 48119 bp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www-seq.wi.mit.edu
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/note="assembly_fragment"
38195. .49220
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/db_xref="taxon:9606"
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18044. .22424
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Db 153230 -TGTTTTTGTTTTTGAGACAGGGTCTCACTCTGTT	290 pLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGl 306	Db 153132 CAAGTGATTCTCCTGCCTTAGCCTCCAGGTAGGTGGGACTACAAGCGTGTGCCCCCCACA 153073  Qy 306 uAspCysAlaGlyLeuIleTyrAlaGlyGlnTrpAs 318  Qy 316 n	152952 GTGTGAG 152946	RESULT 14 AP000915/C LOCUS AP000915 DEFINITION Homo sapiens genomic DNA, chromosome 18p clone:RP11-720L2, complete	sequences. ION AP000915 N AP000915.5 GI:20334314 DS HTG.	SOURCE Homo sapiens DNA, clone:RP11-720L2. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		AL PUDLISE CE 2 (bas RS Hattori Fujiyan	TITLE Direct Submission JOURNAL Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan	(E-mail:hatt Tel:81-45-50 On Apr 26, 2 Loc	source 1. 188439 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="18"	/map="18p" /clone="RP11-720L2" BASE COUNT 54003 a 41134 c 40027 g 53275 t ORIGIN	Alignment Scores: 9.17e-24 Length: 950 score: 954.50 Matches:	Percent Similarity: 58.40% Conservative: 21 Best Local Similarity: 52.62% Mismatches: 53 Query Match: 49.20% Indels: 8 DB: 9 Gaps:	US-09-763-712A-2_COPY_206_547 (1-342) x AP000915 (1-188439)
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Dipublished

Sirren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Badess 1 to 71044)

Sanderson, S., Baddwin, J., Barna, N., Beda, F., Boquslavkly, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Chopel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Grand, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Haoler, N., Grand, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Illev, I., Johnson, R., Johnson, R., Johnson, R., Johnson, F., McCarth, M., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McCurk, A., McKernan, K., McHerter, S., R., Meldrim, J., Meneus, L., Mihova, T., Mranda, C., Marquis, N., McCarthy, M., Pister, Rogov, P., Ronnor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Peterson, K., Pister, Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zinmer, A. and
                                                                                          ACU24368 71044 bp DNA linear HTG 28-FEB-2000
Homo sapiens chromosome 11 clone RP11-179K3 map 11, LOW-PASS
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryotani Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. [ bases 1 to 71044]

Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo. sapiens chromosome 11, clone RP11-179K3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (28-FBB-2000) Whitehead Institute/MIT Center for Genome Submitted (28-FBB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          699 798: gap of 100 bp 799 1495: contig of 697 bp in length 1496 1595: gap of 100 bp 1596 2284: contig of 689 bp in length 1596 2384: gap of 100 bp
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                                                                                                                                                                                                                                                AC024368
AC024368.1 GI:7108157
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                                                                                                                                                                                                                                                                                                          HTG; HTGS_PHASE0.
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                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
Db 44073 GTGTGAG 44067
                                                                                                                                      LOCUS
                                                                                                                                                                                                                                        ACCESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
JOURNAL
                                                                 RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                     AC024368
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10 23709; gap of 100 bp 24402; contig of 693 bp in length 13 24502; gap of 100 bp 25291; gap of 100 bp 100 bp 25291; gap of 100 bp 100 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 13404; gap of 100 bp 14095; contig of 691 bp in length 16 14195; gap of 100 bp 16 14881; contig of 686 bp in length 18 14881; gap of 100 bp 100 bp
                                                                                                                                                                                       100 bp
of 682 bp in length
100 bp
of 674 bp in length
100 bp
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18836: contig of 696 bp in length
18936: gap of 100 bp
19621: contin of 100 bp
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22017: contig of 693 bp in length

2217: gap of 100 bp

22815: contig of 698 bp in length

22915: gap of 100 bp

22609: contig of 694 bp in length
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f 676 bp in length
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25 LysLeuValAspSerLysHisGlyGlnLeuIle-----LysAsnPheThrIleLeu 41
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36 31635; gap of 100 bp 32329; contig of 694 bp in. 31 32429; gap of 100 bp 10 3314; gap of 100 bp 15 33214; gap of 100 bp 16 33214; gap of 100 bp 19 34694; contig of 696 bp in 15 34794; gap of 100 bp 15 3456; contig of 696 bp in 15 35586; contig of 692 bp in 17 35586; contin
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23 contig of 673 bp 10
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39449: contig of 686 bp
39549: gap of 100 bp
40236: contig of 687 bp
40336: gap of 100 bp
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50465: contig of 693 bp
50565: gap of 100 bp
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-Q=Cqqq2_1/VSPC_SPOO_TOSO(976312/runat_14032003_100949_18091/app_query.fasta_1.1877
-Q=Cqqq2_1/VSPC_SPOO_TOSO(976312/runat_14032003_100949_18091/app_query.fasta_1.1877
-DD=N_Geneseq_101002 -QPMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THE_SCOREE=Ct -THR_MAX=100 -THR_MINE - ALIGN=15
-UOCALIGN=200 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09763712_CGCN_11_626_Grunat_14032003_100949_18091 -NCPU=6 -ICPU=3
-NON_XLPX - NO_MMAP -LARGEQUERY -RGS_COCRES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_THREOUT=30 -THREADS=1 -XGADOP=10 -XGADEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/\*tag= a /product= "collectin"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

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The invention relates to polynucleotides encoding a new collectin of human origin. The collectin can be used as an antibacterial and antiviral agent and for screening potential drug molecules. The new collectin can be produced by standard recombinant methodology. The present sequence represents a DNA encoding the human collectin.
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Conservative:
Mismatches:
Indels:
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1449 GCACCGGAGGACAATGGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACTAT 1329 140 849 100 120 161 ProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLysGlyProPro 180 606 40 80 9 SerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLysProGlyProGln LeuGlnGlyProProGlyProArgGlyProArgGlyAspArgGlySerGlnGlyProPro 790 CTACAAGGTCCACGGGCCCCAGGGGTCCAAGAGGTGACAGAGGATCCCAGGGACCCCCT GlyProSerGlyAspProGlyProProGlyProProGlyLysGluGlyLeuProGlyPro 81 AlaGlyGluArgGlyProIleGlyProAlaGlyProProGlyGluArgGlyGlyLysGly GlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGly GlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrPro AlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAspLysCysTyrTyr ArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeu HisLeuValPheIleAsnThrArgGluGluGluGlnGlnTrpIleLysLysGlnMetValGly BP. ABA97932 standard; cDNA; 2262 |||||| |GCATTA 1695 342 141 1210 1270 1390 281 41 101 121 201 241 261 510 301 1570 341 181 1690 RESULT 2 ABA97932 g ΩX q g qq g Db g g a g qq qq q g Q õ óγ δÝ ò δ ò ò δ Ω ò ò g

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Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                            ProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLysGlyProPro
                                                                                                         GlnCysGluAspValAsnAsnPheIleCysGluLysAspArgGluThrValLeuSerSer
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                                                                                                                           GlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrPro
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                                                         scavenger; receptor; diagnosis; treatment; autoimmune disease;
                                                                                                                                                                                                                                                                                                                             The invention relates to a human scavenger receptor-like protein. The protein is useful as a target molecule for diagnosis, prevention and treatment of autoimmune diseases such as rheumatoid arthritis.
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P-PSDB; ABB08642.
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                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the invention relates to human nucleic acids (AAI57798-AAI61369) and the ancoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic catara sclerosas, and Shy-Darger Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotextic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and consistent the sequence data for this patent did not form part of the printed
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                                                                                                                                          Wang
                                                                                                                                                                                                                        for treating disorders
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                                                                                                                                          Ren F,
Zhang J;
                                                                                                                                          Oian XB,
Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              548 G; 504 T; 0 other;
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Mismatches:
                                                                                                                                       Chen R, Ma Y, C
Xu C, Xue AJ,
t, Drmanac RT;
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Matches:
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                                                                                                                                         Chen R,
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                                                                                                                                       Liu C, Asundi V, Che
Wang Z, Wehrman T, Xo
Zhou P, Goodrich R,
        21-JAN-2000, 2000US-0488725.
25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-0620312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0653450.
19-OCT-2000; 2000US-0653450.
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1940.00
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P-PSDB; AAM39686.
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Best Local Similarity:
Query Match:
                                                                                                                 (HYSE-) HYSEQ INC.
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Wang J, W
Zhao QA,
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Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
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963 TCTAAAAGGCTCCCAAGGCCCCAAAGGCTCCCGTGGGAAGCCCCGGCCCTCAG
                                                                                                                                            ArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a human scavenger receptor.
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74..2302
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1694 CAGGGCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGA 1753
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2000US-220644P.
2000US-220644P.
2000WO-US20710.
200UUS-0643657.
2000WO-US25852.
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02-AUG-2000;
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                                                                                                                                                 New Scavenger receptor proteins SRCL-P1 with collectin-like structure, useful for treatment and diagnosis of diseases associated with oxidized low-density lipoprotein accumulation
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Matches:
Conservative:
Mismatches:
Indels:
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                                    2001WO-JP00874
                                                              2000JP-0309068
                                                      2000JP-0035155
                                                                                  (FUSO ) FUSO PHARM IND LTD
                                                                                                                      WPI; 2001-497076/54.
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                                                                                                                               P-PSDB; AAG63346
WO200159107-A1
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                                   08-FEB-2001;
                                                      14-FEB-2000;
                                                               10-OCT-2000;
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                  16-AUG-2001
                                                                                                    Wakamiya N;
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Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antianteriosclerotic; gene; ss.
                                                                                              1873
                 1934 TTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA 1993
                                                                                                                                                                                                                                                                                  2234 CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATCT 2293
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                                                             GlnCysGluAspValAsnAsnPheIleCysGluLysAspArgGluThrValLeuSerSer
ProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLysGlyProPro
                                                                                                                                                                                                PheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGluAspLysSerSer
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Length:

No.:

Pred.

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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycardial infarctions, thromopolhebitis, lymphanditis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paoni NF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothellal or angiogenic disorders in a mammal -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gerber H, Gerritsen ME, Goddard A;
,, Hillan KJ, Marsters SA, Pan J,
.K, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2005 BP; 606 A; 493 C; 491 G; 415 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 27; 567pp; English.
          07-SEP-2000; 2000US-230978EP-2000; 2000US-000000P-18-SEP-2000; 2000US-000000P-18-SEP-2000; 2000US-0065350.

18-SEP-2000; 2000US-0065350.

24-OCT-2000; 2000US-042928-08-NOV-2000; 2000US-0430953.

10-NOV-2000; 2000WO-US30953.

10-DEC-2000; 2000WO-US30953.

20-DEC-2000; 2000WO-US30953.

20-DEC-2000; 2000WO-US30956.

22-JAN-2001; 2000WO-US34956.

28-FEB-2001; 2000WO-US36666.

10-MAR-2001; 2001WO-US06666.

10-MAR-2001; 2001WS-0804208.

10-MAR-2001; 2001US-0804889.

25-MAR-2001; 2001US-0816603.

25-MAR-2001; 2001US-08144.

10-MAY-2001; 2001US-0854208.

25-MAY-2001; 2001US-08544208.

25-MAY-2001; 2001US-0854580.

25-MAY-2001; 2001US-0854603.

25-MAY-2001; 2001US-0854580.

25-MAY-2001; 2001US-0854580.

25-MAY-2001; 2001US-0854580.

25-MAY-2001; 2001US-0854580.

25-MAY-2001; 2001US-0854580.

25-WAY-2001; 2001US-0854580.

25-WAY-2001; 2001US-0854580.

25-WAY-2001; 2001US-0854580.

25-WAY-2001; 2001US-0854580.

25-UN-2001; 2001WS-US317800.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
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STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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FERRARA N.
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Alignment Scores:

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                                                                                  ATGCAACAAGATTTGATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATT
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                Conservative:
Mismatches:
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2.57e-58
1934.00
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                                                                                                                                               hypotensive;
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antiangiogenic;
                                                                                                                                              angiogenesis; cardiant; cytostatic;
                                                                                                                             Human PRO7223 cDNA sequence SEQ ID NO:27.
                                                                              ABL88085 standard; cDNA; 2005 BP.
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2000WO-US20710.
2000US-222695P.
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2000WO-US23328.
2000US-230978P.
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2000WO-US32678.
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2001WO-US06520.
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2001WO-US17800
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18-SEP-2000;
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09-MAR-2001;
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28-JUL-2000;
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ABB88002 to ABL88258 encode the PRO proteins given in ABB84817 to ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic, antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or anglogenic disorder in a mammal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, theresolerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABLBR259 to ABLBR257 represent primers and probes used in the exemplification of the present invention.
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                                                                                                                                                                                      One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGAAGAAATGAAGCTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATA 597
                                             Paoni NF;
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                                           SA, Pan J,
                      Goddard A;
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                                        Marsters SA,
1, Wood WI,
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Indels:
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                 Gerber H, Gerrits
L, Hillan KJ, Mal
SK, Williams PM,
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1934.00
99.71%
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                                           AL, le CK,
Baker KP, Ferrus
Godowski PJ, Gurney AL,
TF, Watanabe CF
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Best Local Similarity:
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(HYSE-) HYSEQ INC.

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1137
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                                                                                                           1438 CAATGTGAAGACGTCAATAACTTCATTTGCGAAAAAGACAGGGAGACAGTACTGTCATTT 1497
                                                                      AlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAspLysCysTyrTyr 220
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                                                                                polynucleotide SEQ ID NO 4617
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2000US-0552317.
2000US-0598042.
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2000US-0653450.
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2000US-0693036
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19-JUL-2000;
03-AUG-2000;
14-SEP-2000;
19-OCT-2000;
29-NOV-2000;
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25-APR-2000;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as lacalised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and CRAS disconcess.
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                        Wang
                                                                                                               Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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                       Ren F, W
Zhang J;
                       Qian XB,
Yang Y,
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Mismatches:
Indels:
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                       , Ma Y, Xue AJ,
                                                Goodrich R, Drmanac RT;
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                    Chen R,
                                    Xu C,
                       Asundi V,
Wehrman T,
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1934.00
99.71%
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                       Liu C, A
Wang 2, V
Zhou P,
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Best Local Similarity:
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                       Tang YT,
Wang J,
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          HisLeuValPheIleAsnThrArgGluGluGlnGlnTrpIleLysLysGlnMetValGly
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                                                      AlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAspLysCysTyrTyr
                                                                            PheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGluAspLysSerSer
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                                 GlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrPro
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23-AUG-1999;
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The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-2, EXMAD-1, EXMAD-5, EXMAD-1, EXMAD-2, EXM
                                                                                                     or
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                                                           Isolated polynucleotide encoding extracellular matrix or adhesion-associated protein (EXMAD) useful for diagnosing, tre preventing disorders associated with expression of EXMAD such proliferative, immune and genetic disorders
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Spaulding V;
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                                                                                                                                                                                                                                                                  ABQ92072 standard; cDNA; 2929 BP.
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LAVALLIE E R.
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SPAULDING V.
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MERBERG D.
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PFSDB; ABPG1859.

XX Wovel secreted or transmembrane protein and polynucleotide encoding the protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis protein, useful for diagnosis and treatment of neurological disorders, cancer, autoimmune diseases, bone disorders and lung or liver fibrosis.

XX The invention relates to human secreted or transmembrane protein (I), their fragments and is encoded by specific complementary decaytibonucleic collem manualian proteins. (I) are useful for preventing, treating or amedical condition, especially immunological treatment or collem manualian proteins. (I) are useful for preventing, treating or amedical condition, especially immunological treatment or collem manualian proteins. (I) are useful for preventing and activity relating to angiogenessis, cytokine, cell proliferation, cell differential for preventing or amedical condition, especially immunological treatment or corrections. (I) can be used to augment or replace activities. (I) can be used to manupulate stance or augment or replace cells damaged by illness, autoimmune disease, accidental damages or genetic disorders. (I) induces the proliferation of neuropathies, such acceptance or peripheral nervous system diseases and neuropathies, such acceptance or septementation of new and branches. (I) is involved in chemotractic or c
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Sequence 2929 BP; 901 A; 699 C; 692 G; 637 T; 0 other;

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Best Local Similarity:
Alignment Scores:
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AlaGlyGluArgGlyPro1leGlyProAlaGlyProProGlyGluArgGlyGlyLyLySGly 100

98US-0087255. 97US-0868696. 97US-0868697. 97US-0868698.

98WO-US11210

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immune suppressor; haematopoiesis regulator; tissue growth; chemotaxis;
activin/inhibin; chemokinesis; haemostasis; thrombolysis;
receptor/ligand activity; anti-inflammatory; tumour inhibitor;
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                                                                                                              1926 TTTTCAGTTGAGAAAGAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCA 1985
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                                                                                                                                                                                                                                     1866 GCACCGGAGGACAATAGCTGCCGCCTCACTGGAAGAACTTCACAGACAAAATGCTACTAT
                                                                                                                                                                                                                                                                                                           HisLeuvalPheIleAsnThrArgGluGluGlnGlnTrpIleLysLysGlnMetValGly
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                                                                                                   GlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGly
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This sequence encodes a human secreted protein of the invention.

This DNA sequence was isolated from a human adult brain cDNA

This DNA sequence was isolated from a human adult brain cDNA

Thisary, and was designated clone bv227_1. The DNAs and proteins

are predicted to have biological activities which would make them

suitable for treating, preventing or ameliorating medical conditions in

humans and animals, although no supporting data is given. Suggested

cutivities include nutritional sources or supplements, immune

stimulating or suppressing activity, haematopolesis regulating activity,

tissue growth activity, activin/Anhibin activity,

chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,

receptor/ligand activity, anti-inflammatory activity, cadherin/tumour

invasion suppressor activity, anti-inflammatory activity, and elusion from activity. The DNAs

are also stated to be useful for gene therapy. A host cell transfected

with the DNA, or its subfragments and variants is useful for recombinant

production of the human secreted protein clones.
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                                                                                                                                                                                                                                                                                                                                                                         New polynucleotides encoding secreted human proteins - derived from human foetal brain, adult brain, foetal kidney, adult ovary, adult retina, adult placenta or adult uterus cDNA libraries
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Mismatches:
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Treacy M;
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970S-0868899
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P-PSDB; AAW73628.
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McCoy JM,
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Location/Qualifiers

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                                                                        GlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGly
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                                                                                                                                                                                                                                                                                                                                                      scavenger receptor; SRCL-P1; macrophage; basal immunity;
                                                                                                                                                                                                                                                                                                                                             Nucleotide sequence of a human scavenger receptor
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arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRCL-P1 with collectin-like structure, sis of diseases associated with oxidized
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Matches:
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useful for treatment and diagnosis of
low-density lipoprotein accumulation
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                                                                                    Location/Qualifiers 92..2320
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                low density lipoprotein;
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                                                                                                                                                                                                                                                                                                                                                                 Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                 AspGlyThrSerProAspTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHis
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                                                                                                                                           221 PheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGluAspLysSerSer
                                                                                                                                                                  HisLeuValPheIleAsnThrArgGluGluGluGlnGlnTrpIleLysLysGlnMetValGly
                                                                                                                                                                                                                          2132 GACGGGTCACCTGTTGATTACAAAAACTGGAAAGCTGGACAACCAGATAACTGGGGCAGT
                                                                        ProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLysGlyProPro
                                                                             GlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrPro
                                                                                                                                                                                                                                                            GlnCysGluAspValAsnAsnPheIleCysGluLysAspArgGluThrValLeuSerSer
                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #6937
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The invention relates to isolated polynuclectide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, colymerase chair reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The cand gene mapping expressed genes (II) is useful in gene therapy techniques of for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving consistency of (II) or to treat disease states involving a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynuclectide sequences have applications in cappositics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and cand to produce other types of data and products dependent on DNA and cand ocid sequences. AASfelf-Arbarbace of the invention.

Conditional sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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Best Local Similarity:
                                                                     (HYSE-) HYSEQ INC
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31-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                 Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
low density lipoprotein; ss.
                                                                                                                                                                                                                                                 GluProThrProAlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAsp 216
                                                                                                                    AsnTrpGlyHisGlyHisGlyProGlyGluAspCysAlaGlyLeuIleTyrAlaGlyGln 316
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                                           GlyValProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyPro 176
                                                                    LysGlyProProGlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsn 196
                                                                                                                                                                                                 TrpLysTrpLeuAspGlyThrSerProAspTyrLysAsnTrpLysAlaGlyGlnProAsp 296
                                                                                                                                              GlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGlu
                                                                                                                                                                                                                                CTCCCCGGCCCTCAGGGCCCTCCTGGCTTCCAGGGACTTCAGGGCACCGTTGGGGGAGCCT
                                                  LeuProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluPro
                                                                                                                                                                                                                                                                                                                                                      Nucleotide sequence of a human scavenger receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                            receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                           "scavenger
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
74..1936
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The present sequence encodes a human scavenger receptor, designated SRCL-P1. The SRCL-P1 polypeptide has a collectin-like structure. They are useful in clarifying the functions of macrophages and basal immunity. They are also useful in the treatment, prevention, diagnosis and investigation of diseases such as arteriosclerosis, dlabetic complications, bacterial infection and restenosis following angloplasty, which are associated with accumulation of oxidized low density lipoprotein and the binding of advanced glycation end-products into
                                                                                                                                                                                                                                                        New Scavenger receptor proteins SRCL-P1 with collectin-like structure, useful for treatment and diagnosis of diseases associated with oxidized low-density lipoprotein accumulation
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Best Local Similarity:
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14-FEB-2000;
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                                                                                                                                Wakamiya N;
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PS Claim 6; Page 142-150; 175pp; Japanese.			CC and diagnosis of diseases in which intracellular stress is important, CC such as arteriosclerosis, diabetic circulatory obstruction, and microbial CC infection. Expression of the proteins is induced in vivo in response to		Sequence 3685 BP; 901 A; 1142 C; 972 G; 669 T; 1 oth nment Scores:	d. No.: 1.07e-10  zre: 540.00  cent Similarity: 66.14  t Local Similarity: 51.85\$	Indels: Gaps: 1-342) x AAX27858 (1-30	Qy 5 LeumetargSerArgLeuAspThrGluValAlaAsnLeuSerValI1eMetGluGluMet 24	Qy 25 LysLeuValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyPro 44	Qy 45 ProGlyProArgGlyProArgGlyAspArgGlySerGlnGlyPrOProGlyProThrGly 64	Oy 65 AsnLysGlyGlnLysGlyGlu	Qy 73 GlyGluProGlyProProGlyProAlaGlyGluArgGlyProIleGlyProAlaGlyPro 92	Qy 93 ProGlyGluArgGlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGly 112	Qy         113 SerProGlyBroGlnGlyProSerGlyAroBroGlyProPro 132	Db   1753GGACAGCCCAAAAGGGGACATAGGGCCCCCAGGGCCAGGGCCCCCG   1806	Qy         153 valGlyGluProGlyValProGlyProArgGlyLeuProGlyLeuProGlyValProGly         172	1867	Db 1927 CTCCGGGGCCTCCAGGTCCAGGA 1953	SULT 15 K27856	1D AAXZ/830 Standard; DNA; 3010 BF. XX AAX27856.	XE:	XX DE Human CSR1 protein coding sequence. XX XW Cellular stress response protein; CSR1; CSR2; CSR3; human; macrophage;
Db 1516 1516	Qy 181 GlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrPro 200	Db 1516 1516	201 AlabroGluAspAsnGlyCysProProHisTrpLysAsnPheThrAspLysCysTyrTyr 2	1517GGCTGCCCGCCTCACTGGAAGAACTTCACAGACAAATGCTACT	<pre>Qy 221 PheServalGluLysGluIlePheGluAspAlaLysLeuPheCysGluAspLysSerSer 240</pre>	Qy 241 HisLeuValPheileAsnThrArgGluGluGluGlnGInTrplieLysLysGlnMetValGly 260 	Oy 261 ArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeu 280 	Qy 281 AspGlyThrSerProAspTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHis 300 	Oy 301 GlyHisGlyProGlyGluAspCysAlaGlyLeuIleTyralaGlyGlnTrpAsnAspPhe 320 	Oy 321 GlnCysGluAspValAsnAsnPheTleCysGluLysAspArgGluThrValLeuSerSer 340 	Oy 341 Alaleu 342                 Db 1922 GCATTA 1927	RESULT 14 AAX27858 ID AAX27858 standard; DNA; 3685 BP.	AAC AAX27858; XX DT 02-JUN-1999 (first entry)	Human CSR	KW Cellular stress response protein; CSR1; CSR2; human; macrophage; KW scavenger receptor protein; intracellular stress; arteriosclerosis; KW diabetic circulatory obstruction; microbial infection; ss. XX Homo sapiens.	3	PD 25-FEB-1999. XX BF 12-AMG-1008. 08460-TE02602	30-JUL-1998; 98JP-023012 13-AHG-1997: 97JP-023339	(NISB ) JAPAN TOBAC	AA PI Nakamura Y, Tokino T; XX	DR WPI: 1999-181032/15. DR P-PSDB; AAY00994.	AAA Scavenger receptor proteins - for treatment and diagnosis of PT disorders involving cell stress XX

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This sequence encodes the human cellular stress response 1 (CSR1) protein of the invention. The CSR proteins are macrophage scavenger receptor proteins. The CSR proteins can be used in the treatment, gene therapy and diagnosis of diseases in which intracellular stress is important, such as arteriosclerosis, diabetic circulatory obstruction, and microbial infection. Expression of the proteins is induced in vivo in response to intracellular stress, and inhibits cell death as a result of such stress.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1530 CTGCTCAGTGCCCGGCTGGACCTCCAACGTCCGGAACCTCTCCATGATCGTGGAGGAGATG 1589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 LeuMetArgSerArgLeuAspThrGluValAlaAsnLeuSerValIleMetGluGluMet 24
scavenger receptor protein; intracellular stress; arteriosclerosis; diabetic circulatory obstruction; microbial infection; ss.
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                                                                                                                                                                                                                                                                                                                           Scavenger receptor proteins – for treatment and diagnosis of disorders involving cell stress
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Matches:
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Mismatches:
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P-PSDB; AAY00992.
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Best Local Similarity:
                                             Homo sapiens
                                                                        WO9909159-A1
                                                                                                                                      2-AUG-1998;
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13-AUG-1997;
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Search completed: March 21, 2003, 08:38:21 Job time : 198.718 secs

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APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
US-09-167-364-1
US-09-449-907-1
US-09-449-907-1
US-09-029-348-20
US-08-749-200-5
US-08-749-200-5
US-08-749-200-5
US-08-749-705-1
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US-09-131-470-3
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US-09-535-521-3
US-09-535-521-4
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US-08-642-255-50
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; Patent No. 5773249
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: ROWLAND, BEFLIAM I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A555
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 494-8701
TELEFAX: (415) 494-8771
TELEFAX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
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CITY: San Francisco
STATE: California
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-Q-/cgn2_1/USPTO_spool/US09763712/runat_14032003_100951_18187/app_query.fasta_1.1877
-DB-1ssued_ratents_NA -OFFMT-fastap -SUFFIX=n1 -MINMATCH=0.1 -LOOPCL=0
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                               GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                            nucleic search, using frame_plus_p2n model
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US-08-1029-348-19
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US-08-655-669-11
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US-08-642-255-48
US-08-159-784-4
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US-08-399-889-1
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Maximum Match 100%
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Maximum DB seq length: 200000000
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Xgapop 10.0 ,
Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Indels:
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Matches:
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ADDRESSEE: DILMORTH & BARRESE
STREET: 333 EARLE OVINGTON BOULEVARD
CITY: UNIONDALE
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                                                   **LECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic"
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Patent No. 5821089
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APPLICANT: BUECHTER, DOUGLAS
APPLICANT: ZHANG, GUANGHUI
APPLICANT: CONNOLLY, KEVIN
NUMBER OF SEQUENCES: 5
                                                                                                             1.74e-17
459.50
53.168
48.958
23.698
LENGTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                        linear
                                                                                                                                         Percent Similarity:
Best Local Similarity:
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                                    TOPOLOGY: 11
MOLECULE TYPE:
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                                                                                                                           APPLICATION NUMBER: US/08/655,086
FILING DATE: 03-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STERN, JEFFREY S.
REGISTRATION NUMBER: 203-1632
REFERENCE/DOCKET NUMBER: 203-1632
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-228-8484
INFORMATION FOR SEQ ID NO: 1:
                                                                       OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                             MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-SOFTWARE: Patentin Release #
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452.50
52.11%
46.48%
23.32%
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
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ZIP: 11553
COMPUTER READABLE FORM:
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Best Local Similarity:
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                                              238 CAGTATGATGGAAAAGGAGTTGGACTTGGCCCTGGACCAATGGGCTTAATGGGACCTAGA
                                                                                              120 GlnGlyProSerGlyAspProGlyProProGlyProProGlyLySGluGlyLeuProGly
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Matches:
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                      103 GlySerGlnGlyProLysGlySerArgGlySerPro-
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TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REPERBNCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                          200 ProAlaProGluAspAsnGlyCysPro 208
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Query Match:
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                                      1424 GAACAAGGCCCTGCTGCTCCCCC---GGATTCCAGGGTCTCCCTGGTCCTGCTGGTCCT 1480
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                                                                                                                                                                                    Sequence 50, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                756
87
6
63
13
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                1481 CCAGGTGAAGCAGGCAAACCTGGTGAACAGGGTGTTCCT 1519
                                                                            --- ProGluAspAsnGlyCysPro 208
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Mismatches:
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NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFRENCE/POCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 50
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448.50
55.03%
51.48%
23.12%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                  STREET: 4 Embarcadero
CITY: San Francisco
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                    US-08-642-255-50
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Db 298 GGCCACCTGGTGCAGCTGGAGCCCAGGCCCTCAAGGTTTCCAAGGACTGGTGAG 357	Qy     111 ArgGlySerProGlyLys       11	Qy 123	Oy 136 GlyLeuProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGlu 155	Oy 156 ProGlyValProGlyProArgGlyLeuPro	<pre>Qy 167 LeuProGlyVal</pre>	Qy 178 GlyProProGlyProSerGly	Oy 188AlaValValProLeuAlaLeuGlnAsnGluProThrProAlaProGluAspAsnGly 206	<pre>Qy 207 CysProProHisTrpLysAsnPheThrAspLysCys 218</pre>	RESULT 5  105-08-159-784-1  105-08-159-784-1  105-08-159-784-1  105-08-159-784-1  105-08-159-784-1  106-08-159-108-1  106-08-08-159-108-1  106-08-08-108-108-108-108-108-108-108-108-1

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APPLICANT: VAUGHAN, Paul R.
APPLICANT: GALANIS, Maria
APPLICANT: RAMSHAW, John A.M.
APPLICANT: WERKMEISTER, Jerome A.
TITLE OF INVENTION: A METHOD FOR PRODUCING, IN YEAST, A HYDROXYLATED TRIPLE
                                                                                                                                                                                                                                                                                                                           1387 recrargeacea---gaacergeageerrecragraracerggaaggaagaaceceee 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1144 GGTTTTCCAGGTCCCCCGGGACTCCAGGTCCT-----CCAGGCAAAGAGGCCCA 1494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1027 GGACCTCAGGGGCCACCAGGGAAGGATGGCACTCCAGGAAGGGATGGTGAACCGGGTGAC 1086
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 SerGlnGlyProLysGlySerArgGlySerProGlyLysProGlyProGlnGlyProSer 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 GlyAspProGlyProProGlyProProGlyLysGluGlyLeuProGlyProGlnGlyPro 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 .......GlyLeuProGlyLeuProGlyValProGlyMetPro 174
                                                                                                                                                                                                                 45
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                                                                                                                                                                                                                                                                                                                                                                                65 AsnLysGlyGlnLysGlyGluLysGlyGluPro-------GlyProProGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1267 GGATCCGGTTTCAGCGGAGACATAGAGAGCCTTAGAGGCCCACGAGGCTTCCCTGGCCCC
                                                                                                                                                                                                               26 LeuValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProPro
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                                                                                                                                                                                                                                                                      46 GlyProArgGlyPro------
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                                                                                                                                                                                     US-09-763-712A-2_COPY_206_547 (1-342) x US-08-159-784-1 (1-4031)
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95
15
49
78
                                                                                                             Conservative:
Mismatches:
Indels:
Gaps:
                                                                                    Length:
Matches:
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                                                                                    4.17e-15
428.00
46.41%
40.08%
22.06%
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-159-784-1
                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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                                                                     Alignment Scores:
Pred. No.:
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US-09-297-269-39
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202 ProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAsp-
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REGISTRATION NUMBER: 8389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3660
TELERAX: 415-854-3660
TELERAX: 66141 PENNE
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2543 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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LOCATION: 47...
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TITLE OF INVENTION: HELICAL PROTEIN, AND YEAST HOST CELLS USEFUL IN SAID TITLE OF INVENTION: METHOD (As Amended)
FILE REFERENCE: Q54094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ArgGlyProlleGlyProAlaGlyProProFigluArgGlyGlyLySelySerLysGly 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 GlyProGlnGlyProSerGlyAspProGlyProProGlyProProGlyLySGluGlyLeu 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    138 ProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGly 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGGCAACCAGGCCCTCCTGGACCTCCTGGTGCCCCTGGTCCTTGCTGCGGTGGTGTTGGA 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                775 GCCGCTGCCATTGCTGGGATTGGAGGTGAAAAAGCTGGCGGTTTTTGCCCCGTATTATGGA 834
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                                                                                                                                                                                                                                                                                                            Length:
Matches:
Conservative:
Mismatches:
Indels:
                                           CURRENT APPLICATION NUMBER: US/09/297,269
CURRENT FILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: P03310
EARLIER FILING DATE: 1966-10-29
EARLIER PILING DATE: 1996-10-29
EARLIER PELICATION NUMBER: P03306
EARLIER PELICATION NUMBER: P07/AU97/00721
EARLIER FILING DATE: 1997-10-29
NUMBER OF SEQ ID NOS: 43
SEQ ID NO 39
                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Collagen Type III Alpha I Chain
US-09-297-269-39
                                                                                                                                                                                                                                                                                                            2.58e-15
424.50
42.48%
35.10%
21.88%
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Best Local Similarity:
Query Match:
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1063 ACTGGGGAAACATGCATAAGTGCCAATCCTTTGAATGTTCCACGGAAACACTGG----- 1116
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                                                                                                                                                                                                                                                                                                                  1003 TGGGTCGACCCTAACCAAGGATGCAAATTGGATGCTATCAAGGTATTCTGTAATATGGAA 1062
                                                                                                                                                                                                                                                               239 -----SerSerHisLeuValPheIleAsnThrArg 248
                                                                                                                                                                                                                                                                                                                                                                      249 GluGluGlnGlnTrpIleLysLysGlnMetValGly---ArgGluSerHisTrpIleGly 267
                                                                                                 883 CTCAAGTCTGTTAATGGACAAATAGAAAGCCTCATTAGTCCTGATGGTTCTCGTAAAAAC 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               268 LeuThrAspSerGluArgGluAsnGluTrpLysTrp-------LeuAspGly 282
835 CCTGAA------CCAATGGATTTCAAAATCAACCGGATGAGATTATCACTTCA
                                            217 ---LysCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLys-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08555669
Patent No. 5773248
GENERAL INFORMATION:
APPLICANT: Brewton, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2543
121
26
                                                                                                                                                         -----LeuPheCysGluAspLys----
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APPLICATION NUMBER: US/08/555,669 FILING DATE: 13-NOV-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
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419.00
35.59%
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Quer DB:	Query Match: 21.60% Indels: 176 DB: 1 Gaps: 9	
ns-c	US-09-763-712A-2_COPY_206_547 (1-342) x US-08-555-669-11 (1-2543	
Oy Op	Qy 27 ValaspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProProGly :::	roGly 46         GGGA 1030
Qy		snLys 66 
QQ	1031	AGAAG 1090
Qy Dp	Qy 67 GlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGlyPro	lyPro 86    
δŷ	87	104
qq	Db 1151 CCTGGAGATGCTGGGGAGCGGGGGGGGCTGGCCACCGGGGCTCAGGGGG	CGGGG 1210
ò à	Oy 105GlnGlyProLys	roLys 108
3 8	109	128
g 20	1271	
Qy	Qy 129 ProGlyProProGlyLgluceuProGlyProGlnGlyProFroGlyPheGlnGly	lnGly 148 
qq	1331	ACGGT 1390
ò d	Qy 149 LeuGlnGlyThrValGlyGlu	
3	1 L	
Š i	CCT	
g	1451	GTGTT 1510
ò		roGly 172
Op	1511	cresc 1570
δy	Qy 173 Met	173
QQ	Db 1571 ATCACGGGGAAGCCGGGAGTTCCGGGGAAGGAGGCCAGCGAGCAGCAGCATCAGGGAGCTG	AGCTG 1630
δy	Оу 173	173
Dp	Db 1631 TGTGGGGGGATGATCAGCGAACAAATTGCACAGTTAGCCGCGCACCTAAGGAAGCCTTT	CTTTG 1690
Ολ		
qq	1691	ccccA 1750
δy	187	198
С	1751	GGGAG 1810
Qy	199	Thras 216
qq	Db 1811 CTGGGAGCCCGGGCCCAGAG	1832
ò	Qy 216 pLysCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGl	CysGl 236
Q.	1833GAAACCAGGGTGACAGAG	1859
δλ		sLy 2
g	1860	1874

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1972 GCCTCCCGGAGATCCTGGGCTTCCAGGTGCCATTGGGGCCCCAGGGGACACCGGGGATCTG 2031
                                                                   276 uTrpLysTrpLeuAspGlyThrSerProAspTyrLysAsnTrpLysAlaGlyGlnProAs 296
256 sGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGl 276
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Sequence 11, Application US/09073663

Sequence 11, Application US/09073663

GENERAL INFORMATION:

APPLICANT: Brewton, Richard

APPLICANT: Mayne, Richard

TITLE OF INVENTION: 17FE IX COLLAGEN AND FRAGMENTS THEREOF

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: McGregor & Adler, LLP

STREET: 8011 Candle Lane

CITY: Houston

STATE: Texas

COUNTRY: USA

21P: 77071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-763-712A-2_COPY_206_547 (1-342) x US-09-073-663-11 (1-2543)
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121
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176
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                        296 pAsnTrpGlyHisGlyHisGlyProGly------
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MEDIUM TYPE: FLOPPY disk
COMPUTER: APPLE Macintosh
OPERATING SYSTEM: Macintosh OS 8.1
SOFTWARE: Microsoft WORD for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,663
FILING DATE:
CLASSIFICATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: D5913D
REGISTRATION NUMBER: D5913D
TELEFONMUNICATION INFORMATION:
TELEPHONE: (713) 777-6908
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHRRACTERISTICS:
LENGTH: 2543 base pairs
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 11:
STRANDEDNESS: unknown
MOLEGULE TYPE: CDNA
FEATURE:
CNAME/KFY: CDS
                                                                                                                                                                                                                                2032 CGACACCTCAGCCTGCCAAGGAGCCGTGTTAGGAGGG 2068
                                                                                                                                                                                                            306 -----GluAspCysAlaGlyLeuIleTyrAlaGly 315
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29.30%
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Best Local Similarity:
Query Match:
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LOCATION:
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Qy 296 pAsnTrpGlyHisGlyHisGlyProC	ZAN ZAN ZES ZES ZES ZES	ZIP: 94111-4187  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS: SOFTWARE: PALENTIN Release CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/66 FILING DATE: CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: ROWLAND, BETLAM I. REGISTRATION NUMBER: Z0,015	REFERENCE/DOCKET NUMBER: A55  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 494-8771  TELERA: (415) 494-8771  TELERA: 910 277299 FHT UR  TROPMATION FOR SEQ ID NO: 48: SEQUENCE CHARACTERISTICS: LENGTH: 432 base pairs TYPE: nucleic acid STRANDENESS: double STRANDENESS: double TOPOLOGY: linear MOLECULE TYPE: other nucleic & US-08-642-255-48	Alignment Scores:
986 CTCGATGGCCAGAAGGGAGGCTGGTCGCAACGGTGCTCCGGGA 1030 47 ProArgGlyProArgGlySerGlnGlyProProGlyProThrGlyAsnLys 66 51 :::	CCCTCGGCCCACAAGGCCCTCGGAGCCCTGGTGTCCCACGGGGCTCTCCAGGGCCTCCACGGGGCCTCCAGGGCCTCCAGGGCCTCCAGGGCCTCCAGGGCCTCCAGGGCCTCCAGGGCCTCCAGGGCCTCCAGGGCCTCCAGGGCCTCCAGGGCCTTCCAGGCCCCCAGGGCCTCCCAGGGCCTTCCAGGCCCCCAGGGCCTCCCAGGGCCTTCCAGGCCCCCAGGGCCTCCCAGGGCCTCCCAGGTGCCGAGGCCCTCCAGGCCCCCAGGGCCTCCCAGGTGCCGTGCCCAGGCCCTACAGGCCCCAGGGCCTCCCAGGTGCCGTGCCCAGGCCCAGGGCCTCCCAGGCCTACAGGCCCAGGGCCTACAGGCCCAAGGCCCTAAGGGCCCCAAGGCCTAAGGGCCCTAAGGGCACCCAGGGTTCCCACGGTCCCACGGTCCCACGGTTCCCACGGTTCCCACGGTTCCCACGGTTCCCACGGTTCCCACGGTTCCCACGGTTCCCACGGTTCCCACGGTTCCACGCTTCACACGCTACACGCTACACGCTACACGCTACACGCTACACGCTACACCACACACA	149   LeuGlnGlyThrValGlyGlu	173 Met	199ThrProAlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAs 216
DP OA		0y 0y 0y 0y		

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|AGGTGCCATTGGGGCCCAGGGGACACCGGGGATCTG 2031
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ecular Weight Collagen-Like
Polymers
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Ser, Suite 3400
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se #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CGTGTTAGGAGGG 2068
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US-09-763-712A-2_COPY_206_547 (1-342) x US-08-159-784-4 (1-3394)
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                         291
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                                                                                                                                    ProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArg 162
                                                                                              123 SerGlyAspProGlyProProGlyProProGlyLysGluGlyLeuProGlyProGlnGly
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86
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58
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Patent No. 5643783
GENERAL INFORTION:
GENERAL INFORTION:
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS: ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.

ZIP: 0.110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
COMPUTER: IBM PS/2 Model 502 or 555X
SOFTWARE: WordPerfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
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                                                                                                                                                                                                                                              183 ProGlyProSerGlyAlaValValPro 191
                                                                                                                                                                                                                                                                       403 AAAGGAGCTCACGGTCCGGCAGGTCCG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELERAX: (617) 542-6070
TELEEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29,066
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ATTORNEY/AGENT INFORMATION:
NAME: JOHN F. Freeman
REGISTRATION NUMBER: 29,C
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  409.00
48.98%
43.88%
21.08%
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STATE: Massachusetts
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PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
Query Match:
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US-08-159-784-4
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946 CCTCAGGGACCCCCCGGCATC---GGCTACGAGGGCGCCCAGGGCCCTCCCGGCCCCCCA 1002
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------GGCCCTCCAGGACCCAAGGGCCCCAAAGGAGAAGTG 705
                                                                                                                                                                                                                                                                                                                      96 ArgGlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGlySer----- 113
                                                                                                                                                                                                                                                                                                                                                                                                               -----ProGlyLysProGlyProGlnGlyProSerGly 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 AspProGlyProProGlyProProGlyLysGlu-------GlyLeuProGly 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             886 TACCCTGGGATTCCAGGTCCCAAGGGAGAGCATCCGGGGCCAGCCGGCCCACCTGGA 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 ProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValPro 159
                                                                                              67
                                                                                                                                                                                          87
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APPLICANT: Reeders, Stephen T., Morrison, Karen E., Hudson, Billy
APPLICANT: G.
                                                                                              ---GlnGlyProProGlyProThrGlyAsnLysGly
                                                                                                                         613 AGCAATGTGTTTGCTGAGTCCAGCGCCCCCGGGCCTCCAGGATTGCCAGGAATCAG---
                                                                                                                                                                                          68 GlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGlyProIle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen
TITLE OF INVENTION: Polynucleotides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Vale University, Office of Cooperative Research
STREET: 246 Church Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 800K storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11/30/90
CLASSIFICATION: 424
PRIOR APPLICATION DATA: NO. 5424408 applicable
ATTORNEY, AGENT INFORMATION:
NAMME: AATH, Richard S.
REGISTRATION NUMBER: 28180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 GlyProArgGlyLeuProGlyLeuProGly------
                                                                                                                                                                                                                                                                                      88 GlyProAlaGlyProProGlyGlu-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/621,091G
FILING DATE: 11/30/90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 28180
REFERENCE/DOCKET NUMBER: 900983/RB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh OS7.0
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/07621091G Patent No. 5424408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New Haven
STATE: Connecticut
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; NAME/KEY: CDS
; LOCATION: (1)
US-08-399-889-1
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                                                                                                                                                                                                                                                                       US-08-399-889-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyVal 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 ProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLysGly 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   292 GGTGTCCCCGGTCAGCCAGGGCCAGAGGTGATCCTGGATTCTATGGATTTCCAGGCATG 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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103
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103
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                 CHROMOSOME/SEGMENT: NO. 5424408 known PUBLICATION INFORMATION: NO. 5424408e
                                                                                                                                                                                                                                                         LIBRARY: Bovine lens cDNA
CLONE: KMC15
POSITION IN GENOME: NO. 5424408 known
                                                                                                                                                                                           STRAIN: Unknown
INDIVIDUAL ISOLATE: Unknown
DEVELOPMENTAL STAGE: Unknown
CELL TYPE: Whole kidney
                                 TELEX: 236268
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1416 base pairs TYPE: Nucleic acid STRANDEDNESS: Double TOPOLOGY: Linear MOLECULE TYPE: CDNA to mRNA
TELECOMMUNICATION INFORMATION:
            TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
                                                                                                                                                                                                                                                                                                                                                                 3.6e-14
402.50
46.62%
38.72%
20.75%
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N
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STRAIN: Unknown
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Best Local Similarity:
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                                                                                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                      ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                        TELEFAX:
TELEX: 2
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    -ProHisTrpLysAsnPhe
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| Patent No. 5973120|
| CENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: Recders, Stephen T
| APPLICANT: Morrison, Raren E
| APPLICANT: Hudson, Billy G
| TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
| FILE REFERENCE: 951263A
| CURRENT APPLICATION NUMBER: US/08/399, 889B
| CURRENT FILING DATE: 1995-03-07
| EARLIER APPLICATION NUMBER: 07/621091
| EARLIER FILING DATE: 1990-11-30
| NUMBER OF SEQ ID NOS: 25
| SOFTWARE: PatentIn Ver. 2.0
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Best Local Similarity:
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 352 AAAGGGAAGAAGGGTAATTCAGGATTTCCAGGACCACCTGGACCTCCAGGGCAAAGTGGA 411
                                                                   412 CCAAAAGGACCACCTGGAGTACGTGGAGGCCTGGCACAGTGAAGATCATCTCCCTTCCA 471
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US-09-167-364-1
US-09-167-364-1
Sequence 1, Application US/09167364
Patent No. 6007980
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T
APPLICANT: Morrison, Karen E
TITLE OF INVENTION: Billy G
TITLE REFERENCE: 951263B
CURRENT FILING DATE: 1998-10-07
EARLIER APPLICATION NUMBER: US/09/167,364
CURRENT PILING DATE: 1998-10-07
BARLIER FILING DATE: 1995-03-07
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin Ver: 2.0
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Best Local Similarity:
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LOCATION: (1).
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APPLICANT: Hudson, Billy G
APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REPERENCE: 95-1263-C
CURRENT APPLICATION NUMBER: US/09/439,897
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEO ID NOS: 65
SOFTWARE: PATENTIN Ver. 2.0
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Patent No. 6277558
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ORGANISM: Bos taurus
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LENGTH: 1416
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Query Match:
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US-09-484-970B-4
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                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6426186 331365 (1553795CB1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 LeuGlnGlyProProGlyProArgGlyProArgGlyAspArg-----
                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative:
Mismatches:
Indels:
                                APPLICANT: Jones, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
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400.50
54.89%
48.91%
20.64%
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FEATURE:
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Best Local Similarity:
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                 GENERAL INFORMATION:
APPLICANT: Jones,
6426186
                                                                                                                                                                                                SEQ ID NO 4
LENGTH: 4359
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Sequence 762, App Sequence 782, App Sequence 3946, App Sequence 2094, App Sequence 206, App Sequence 22, App Sequence 22, App Sequence 42, App Sequence 42, App Sequence 388, App Sequence 388, App Sequence 1138, App Sequence 255, App Sequence 2178, App Sequence 255, App Sequence 2178, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64, Appl
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COMPUTER: IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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US-09-902-941-1138

US-09-954-531-961

US-09-954-531-961

US-09-919-497-7

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US-09-915-343-1517

US-09-925-302-64
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US-09-978-697-613
US-09-998-82A-613
US-09-998-189-613
US-10-174-590-331
US-10-176-788-331
US-10-175-737-331
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US-10-175-738-331
US-10-176-482-331
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STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jacobs, Kenneth
MCCOy, John M.
LaVallie, Edward R.
Collins-Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 198, Application US/09745763 Patent No. US20020065394A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Merberg, David
Treacy, Maurice
Spaulding, Vikki
? INVENTION: SECHTED P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evans, Cheryl
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ADDRESSEE: Genetic
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       ZIP: 02140
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    TITLE OF
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-NCPL=5 -ICPU=3 -NO_XMPX -NO_MMPA -LARGEQUERY -NGC_SCORES=0 -WAIT -LONGLOG
-DBV_TIRECUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Sequence 2274, Ap
Sequence 57, Appl
Sequence 57, Appl
                                                                                                                                                                 08:23:12; Search time 166.172 Seconds (without alignments) 1596.010 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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                             5.1.4_p5_4578
Compugen Ltd.
                                                                                                                    nucleic search, using frame_plus_p2n model
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US-09-954-456-2274
US-09-924-340-57
US-09-992-600A-57
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                           version :
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                      0.5
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, Ygapext
, Fgapext
, Delext
                           GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB seq length: 0
DB seq length: 2000000000
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Ygapop 10.0 ,
Fgapop 6.0 ,
Delop 6.0 ,
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Database

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Fotal number

Minimum Maximum

Searched:

Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

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Matches:
Conservative:
Mismatches:
Indels:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/745,763
FILING DATE: 18-Jun-2000
FLING DATE: US-Jun-2000
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                   NO: 198
                                                                                                                                                                                                                                                                                Gaps:
                                                    NAME: Sprunger, Suzanne A.
REGIZHRATION NUMBER: 41,323
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8284
TELEPHONE: (517) 876-881
'ORMATION FOR SEQ ID NO: 198:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                             LENGTH: 2930 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                         2.49e-95
1934.00
99.71%
99.71%
                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                            US-09-745-763-198
                                                                                                                                                                                                                Alignment Scores:
                                                                                                          INFORMATION
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Sets
FILE OF INVENTION: Sets
FILE OF INVENTION: Sets
FILE REPERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/60/233,617
PRIOR PAPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR PELICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR PELICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-26
PRIOR PELICATION NUMBER: US/60/235,637
PRIOR PELICATION NUMBER: US/60/235,637
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,711
PRIOR PELICATION NUMBER: US/60/235,720
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
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49.678
36.278
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US-09-954-456-2274
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Best Local Similarity:
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US-09-954-456-2274
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LENGTH: 1410
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GENERAL INFORMATION: APPLICANT: Bejanin, Stephane APPLICANT: Tanaka, Hiroaki TITLE OF INVENTION: HUMAN CDNAS; FILER REFERENCE: 91.052.REG CURRENT APPLICATION NUMBER: US/ CURRENT FILING DATE: 2001-08-0; PRIOR PELLOR DATE: 2001-06-29 PRIOR FILING DATE: 2001-06-29 PRIOR PELLING DATE: 2001-06-29 PRIOR PELLING DATE: 2001-06-29 PRIOR APPLICATION NUMBER: US 60; PRIOR APPLICATION NUMBER: US 60; PRIOR APPLICATION NUMBER: US 60; PRIOR PILING DATE: 2001-05-25 PRIOR APPLICATION NUMBER: US 60; PRIOR FILING DATE: 2001-05-25 PRIOR PILING DATE: 2001-05-25 PRIOR APPLICATION NUMBER: US 60; PRIOR FILING DATE: 2001-05-25 PRIOR FILING DATE: 2001-05-25 PRIOR FILING DATE: 2001-05-25 PRIOR FILING DATE: 2001-05-25 PROGANISM: Homo sapiens PRAME/KEY: TOPY CCATION: 9651133 CCCATION: 11011106 NAME/KEY: POLYA_Signal LOCATION: 11	US-09-763-712A-2_COPY_206_547 (1-3)   QY
10.00   1.00	Db 930 CTTCCCAAATGGCCAAAGTGTCGGGGAAGATTTCAAGACAGCAGCTTTGTAAAACC 989  Oy 227 ePheGlubaspalatystatTTCAAGACAGCAGGCTTTGTAAAACC 989  Oy 227 ePheGlubaspalatystatTTCAAGACAGGCTTGTCGTCTCTCTTTTTTTTTTTTTTT

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GGATGGTTTGGATGGGATGGCAAGCCTGGCTTG 439
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
            S/09/924,340
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60/305,456
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US-09-763-712A-2_COPY_206_547 (1-342) x US-09-992-600A-57 (1-1133)
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     680 ATCTCTGCAGTGGGTCTGAAAGGAGCAGCGAGCCCACCGGAGAAAGGGGCCTTGCAGGC 739
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GAPLICANT: Benjanio, Stephane

APPLICANT: Tanaka, Hiroaki

TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

FILE REFERENCE: 91.034.DIV

CURRENT PELICATION NUMBER: US/09/992,600A

CURRENT FILING DATE: 2001-11-13

PRIOR PELICATION NUMBER: PCT/IB01/01715

PRIOR PELICATION NUMBER: PCT/IB01/01715

PRIOR PELICATION NUMBER: US 60/305,456

PRIOR FILING DATE: 2001-08-06

PRIOR PILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

PRIOR FILING DATE: 2001-06-15

SEQ ID NO ST

**SECTANES**

**SECTANES**

**PRIOR FILING DATE: 2001-06-15

**PRIOR FILING DATE: 
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Mismatches:
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                                                                                   165 ProGlyLeuPro------
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) LOCATION: 1118..1133
US-09-992-600A-57
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FEATURE:
NAME/KEY: polyA_sign
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Query Match:
DB:
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LOCATION: 476..964
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US-09-992-600A-57
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81 AlaGlyGluArgGlyProlleGlyProAlaGlyProProGlyGluArgGlyGlyLysGly 100
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                                                                                                        145 GlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGlyLeu
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Patent No. US20020106662A1

GENERAL INFORMATION:

APPLICARY: Mutter, George L.

TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
FILE REPERENCE: B0001/7225

CURRENT APPLICATION NUMBER: US/09/919,497

CURRENT FILING DATE: 2001-07-31

PRIOR APPLICATION NUMBER: US 60/221,735

PRIOR FILING DATE: 2000-07-31

NUMBER OF SEQ ID NOS: 100
                                                                                    61 GlyProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyPro
                                                                                                                                                                                           133 -----GlyLysGluGlyLeuProGlyProGln-------GlyProPro
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NAME/KEY: Unsure

LOCATION: (2434)..(2434)

OTHER INFORMATION: n = a,

US-09-919-497-6
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ORGANISM: Homo sapiens
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Alignment Pred. No.:	Scores: 3.35	5e-16	Length:	6158		ფ <u>ი</u> ბ	4849	-CAG
Score: Score: Percent Similari Best Local Simil Query Match: DB:	453 ty: 39. arity: 30. 23.	000 11 8 8 8 0 20 8 8 8 8 0	Matches: Conservative: Mismatches: Indels: Gaps:	: 130 : 38 160 180		7 A 8		CTCA CTCA TVal
.712	US-09-763-712A-2_COPY_206_547	(1-342)	x US-09-919-497	97-6 (1-6158)		qa .	4	
G1.y GGA	ProProGlyProArg(             CCTCCAGGTGCCAAG	GlyProArgG         GGGCGCCAGG	lyAspArgGlySei        3TGATGATGGCCC	GlyProProGlyProArgGlyAspArgGlySerGlnGlyProProGlyPro	, 62 , 4091	qa qa	278 5027	S STrp
63 Thr-		1				QY		
4092 GT	rggttttcctggagatu	CCTGGTCCTC	CTGGGGAACTTGG	GTIGGTTTICCTGGAGATCCTCGTCCTCCTGGGGAACTIGGCCCTGCAGGTCAAGATGGT	4151	qa .	ഗ	
64 4152 GT	GlyAsnLysGly(     :::       TGGTGGTGACAAGGGT	GlnLysGlyG::::    ::  GAGATGGAG	luLysGlyGluPro ::    :::    ATCCTGGTCAACC	GlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProBroGlyProAla	. 81	da da		
82 G1 12 G0	.yGluargGlyProIle(        TGAGGCTGGCCCACCA	Glypro          GTCCTCCTG(	AlaGlyPro         SAAACGAGGTCC	GlyGluargGlyProIleGlyProAlaGlyProProGlyGluargGlyGly	98	y d	331 5152	L uLys
99 Ly :: 72 GP	'sGlySerLysGlySer ::    ::    \GGGAAGACAAGGTGAA	GlnGlyProLy :::    AAAGGTGCTAA	ysGlySerArgGly        AGGGGGAAGCAGG	LysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLySPro 	117	RE US	RESULT 6 US-09-954-456- ; Sequence 762 ; Patent No. U	1-456 3e 76 No.
118 - 4332 A	Gly          AAACCGGCCCAGTCGGT	ProGlnGlyPi                CCTCAGGGAC(	roSerGlyAspPrc   :::        TGCAGGAAAGCC		128 : 4391		GENERAL INFO APPLICANT: TITLE OF IN	ANT: ANT: OF I
· 0	ProglyProPro           GCATCCTGGTCTGTG	GlyLysGluG    :::::  GGAGAACAAGG	lyteu        srcrccrggagg	ProGlyProProGlyLySGluGlyLeu	137		FILE REFERE CURRENT APE CURRENT FII PRIOR APPLI	REFER VT AP VT FI APPL
₽ — D	roGlyProGlnGlyPro             CTGGTCCTATGGGACCT	ProglyPhe         CCTGGCTTACC	CTGGTCTCAAAGG	ProglyProglnGlyProProGlyPhe	146 . 4511		PRIOR PRIOR PRIOR PRIOR	FILIN APPLI FILIN APPLI
t		1			146		PRIOR PRIOR	FILIN
g	AAAAGGGACATCCTGGT	TTAATTGGCC	rgattggtcctcc	GAAAAGGGACATCCTGGTTTAATTGGCCTGATTGGTCCTCCAGGAGAAAAAAAA	4571	•• ••	PRIOR	APPLI
' Ö	GlnGlyLeuGlnGlyThrValGlyGluPro- :::	GlyThrvalg           GAACTCAAG	lyGluPro     SATCTCCAGGAGC	GlnGlyLeuGlnGlyThrValGlyGluProGlyval :::	. 158 . 4631		PRIOR PRIOR PRIOR	
<u> </u>	ProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLys 	ProGlyLeuPi       TTAGGTCCAC	roGlyValProGly         TGGTCCTCCAGG	ProGlyProArgGlyLeuProGlyValProGlyMetProGlyProLys	177 : 4691			
•			1		177			
Ū	CAAAGGGTAACAAAGGC	TCTACTGGAC	CCCTGCCCAGAA	CCAAAGGGTAACAAAGGCTCTACTGGACCCGCTGGCCAGAAAGGTGACAGTGGTCTTCCA	4751		PRIOR FILIN NUMBER OF S	FILIN
0 <del>-</del> 0	lyProProGlyProPro 	GlyProserG          GTCCACCTG	lyAlaValValPro          ::: STGAAGTCATT	GlyProProGlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGlu	1 197 : 4793		SOFTWARE: E SEQ ID NO 76 LENGTH: 61 TYPE: DNA	NE: F NO 76 FH: 61
P - D	ProThrPro-AlaProGl-	uAspAsnGly(	YCysProProHisTrpLys)             -TGTCCTCCAAAAAACGA	ProThrPro-AlaProGluAspAsnGlyCySProProHisTrpLysAsnPheThrAspLy 	. 217		FEATURE: NAME/KEY: OTHER INFO	JRE: /KEY:
ا ش	sCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLysLeuPheCy 	lGluLysGlu	IlePheGluAspA        GAAGACA	GluAspAlaLysLeuPheCysGluAs          GAAGACATACTGAAGGCATGCAAG	, 237	OS Pr	US-09-954- Alignment Pred. No.:	t-456- t Scor
237 pt	<pre>pLysSerSerHisLeuValPhelleAsnThrArgGluGluGln- ::: :::</pre>	LeuValPheIleAsn' ::::::   ::	ThrargGluGluG		. 251		Score: Percent Simila Best Local Sin	Simil sl Si

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LINVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C INVENTION: Sets
OF INVENTION: Sets
OF INVENTION: Sets
REPRENCE: 689290-76
NUT FILID STATE: 2001-09-18
NUT FILID DATE: 2001-09-18
REPLICATION NUMBER: US/60/234,052
FILING DATE: 2000-09-26
REPLICATION NUMBER: US/60/235,134
FILING DATE: 2000-09-25
APPLICATION NUMBER: US/60/235,134
FILING DATE: 2000-09-25
APPLICATION NUMBER: US/60/235,637
FILING DATE: 2000-09-26
APPLICATION NUMBER: US/60/235,710
FILING DATE: 2000-09-26
APPLICATION NUMBER: US/60/235,720
FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,840
FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,840
FILING DATE: 2000-09-27
APPLICATION NUMBER: US/60/235,863
FILING DATE: PALENTH NUMBER: US/60/235,863
                                                                                                                                                                                                                                                                               TGGT------5GTGAGACTTGC----- 5105
CAGATGCAGATGATAATATTCTTGATTACTCGGATGGAATGGAAGAAATATTTGGTTCC 4907
                                                                                     1GlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLy 278
                                                                                                                                                                                                                                                                                                                                                                                                  aGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGluAspCysAlaGlyLe 311
                                                           -----GlnTrpIleLysClnMe 258
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Matches:
Conservative:
Mismatches:
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US20020115057A1
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258 tValGlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLy 278

Query DB:	Mat	ch:	23.35% 10	Indels: Gaps:	180 18	
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Qy Dp	43		GlyproproglyproargGlyProargGlyaspargGlySerGlnGlyProProGly                 :::	31yAspArgG1ySerG          3GTGATGATGCCCTP	Pro     CCT	62 4091
0y	63	Thr		,		63
qq	4092		SGAGATCCTGGTCCTC	CTGGGGAACTTGGCC	GTTGGTTTTTCCTGGAGATCCTGGGTCCTGGGGAACTTGGCCCTGCAGGTCAAGATGGT	4151
Oy Dp	64		LysGlyGlnLysGlyG 	<pre>sluLysGlyGluProG :::     :::     sarccredercaaccec</pre>	GlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAla	81
o o	82		GlyGluArgGlyProlleGlyPro HIIII	AlaglyProF		98
οy	66		SlySerGlnGlyProl	ysGlySerArgGlys		117
QQ	4272		:::        GTGAAAAAGGTGCTA	  AGGGGAAGCAGGTG	:::    :::    :::	4331
9 9	118		GlyProGlnGlyF 	roSerGlyAspProG    :::     CrGCAGGAAAGCCTG		128
ργ	129		ProGlyProProGlyLysGluGlyLeu	lyLeu		137
qq	4392		:::::   CTGTGGGAGAACAAG	  GTCTCCCTGGAGCTG		4451
δo 1	138		ProGlyProGlnGlyProProGlyPhe-		ProGlyProGlnGlyProProGlyPhe	146
g (	4452		SGACCTCCTGGCTTAC	CTGGTCTCAAAGGTG		4511
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qq	4512		CTGGTTTAATTGGCC	TGATTGGTCCTCCAG	GAAAAGGGACATCCTGGTTTAATTGGCCTGATTGGTCCTCCAGGAGAACAAGGGGAAAAA	4571
ò	147	.::	CeuGlnGlyThrValG	31yGluPro	GlydlyLeuGlnGlyThrValGlyGluProGlyVal	158
Dp	4572		rccredaacrcaae	GATCTCCAGGAGCAA		4631
oy G	159		ProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLys	roglyvalProglyM         ctggtccrccAggct	360	177
ογ	177					177
q	4692		AAAGGCTCTACTGGAC	CCGCTGGCCAGAAAG	CCAAAGGGTAACAAAGGCTCTACTGGACCCGCTGGCCAGAAAGGTGACAGTGGTCTTCCA	4751
ç q	178		GlyProProGlyProBroGlyProSerGlyAlaValVal 	:lyAlaValValProL     CTGAAGTCATT	GlyProProGlyProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGlu	197 4793
δ	198		aProGluAspAsnGly	CysProProHisTrp		217
QQ	4794	CCTTTACCAATCT-		TGTCCTCCAAAAAA	.cgA	4824
δŏ	217	sCysTyrTyrPhe	sSerValGluLysGlu	IlePheGluAspAla 	Ø	237
QQ	4825		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GAAGACATA	TGAAGGCATGCAAG	4848
ç q	237	pLysSerSerHis::::	PLYSSerSerHisLeuValPheIleAsnThrArgGluGluGln- :: ::::::::::::::::::::::::::::::::::	ThrArgGluGluGln         acrcGGarGGAATGG	AGA A A TATA GAPA CA	251
δ	252			Gln		258
QQ	4908		AAACAAGACATCGAGC	  atatgaaatttccaa		4967

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Sequence 782, Application US/09954456
Patent No. US200220115057A1
CENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE PERERENCE: 689290-76
                                                                                            4968 CCA-GCCCGAACTTGTAAAGACCTGCAACTCAGCCATCCTGACTTCCCAGATGGTGAATA 5026
                                                                                                                                                                                                                                                                                                                                291 sAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGluAspCysAlaGlyLe 311
                                                           278 sTrpLeuAsp-----GlyThrSerProAsp-----TyrLysAsnTrpLy 291
                                                                                                                                                                                                                                                                                            311 ulleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspValAsnAsnPheIleCysGl 331
                                                                                                                                                                                                                    5087 ATCTGGT-------GGTGAGACTTGC-----
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 003-09-18
PRIOR FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
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PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
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CORGANISM: Homo sapiens
US-09-954-456-782
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Query Match:
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Sequence 786, Application US/09954456
Fatent No. US20020115057a1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/954,456
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/33,617
FRICH REPLICATION NUMBER: US/60/233,617
FRICH REPLICATION NUMBER: US/60/234,052
FRICH REPLICATION NUMBER: US/60/234,923
FRICH RELING DATE: 2000-09-18
FRICH RELING DATE: 2000-09-26
FRICH FILING DATE: 2000-09-26
FRICH FILING DATE: 2000-09-26
FRICH FILING DATE: 2000-09-26
FRICH FILING DATE: 2000-09-26
FRICH RELING DATE: 2000-09-27
FRICH FILING DATE: 2000-09-27
                                                                                           2016 GAACAAGGCCCTGCTGGCTCCCC---GGATTCCAGGGTCTCCCTGGTCGCCTGGTCGTCTT 2072
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                                    US-09-763-712A-2_COPY_206_547 (1-342) x US-09-880-107-3946 (1-6728)
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                                                                                         2016 GAACAAGGCCCTGCTGGCTCCCCC---GGATTCCAGGGTCTCCCTGGTCCTGCTGCTGGTCCT 2072
                                  1545 GGACCCACTGGCCTGCCCGGACCCCCTGGCGAGCGTGGAGCTGGTAGCCGTGGTTTC 1604
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Fatent No. USZ0020142981A1
GENERAL INFORMATION:
APPLICANT: HORNE, Darci T.
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
TITES OF INVEWTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT APPLICATION NUMBER: US/09/880,107
FRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2000-06-14
SPRIOR FILING DATE: 2000-10-02
SOFTWARE PATENTING DATE: 2000-10-02
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ORGANISM: Homo sapiens
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US-09-880-107-3946
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LENGTH: 6728
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                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
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PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR PLLING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR APPLICATION NUMBER: US/60/235,863
NUMBER OF SEQ ID NOS: 2276
SOFWARE: Patentin version 3.0
LENGTH: 5416
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47.15%
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22.89%
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Best Local Similarity:
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2564 GCTGGTCCTGCTGGTCCTCGGGGAAGCCCTGGTGAACGTGGCGAGGTCGGT 2623
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APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Ecglc, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
FILE REFERENCE: 44921-5028 WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT PILING DATE: 2000-106-14
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SOD IN 083: 3950
SOFTWARE: PATENTIN VET. 2.1
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US-09-880-107-2094
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Matches:
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Mismatches:
Indels:
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Best Local Similarity:
Query Match:
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                                          206 GlyCysPro
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LENGTH: 5416
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1667 GGNGACCAAGGACCAGCAGGCCGACCTGGAGAAGTAGGAGCACCGGGTCCCCTGGCTTC 1726
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 85 GlyProIleGlyProAlaGlyProProGlyGluArgGlyGlyLysGlySerLysGlySer 104
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                                 1487 GGCCCNNNNGGTCCAAATGGTCCCCCGGTCCTGCTGGAAGTCGTGGTGGTGATGGAGGCCCC
                                                               105 GlnGlyProLysGlySerArgGlySerProGlyLysProGlyProGlnGlyPro----
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APPLICANT: Horne, Darci T.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liv
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US, 00/99/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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; GENERAL INFORMATION:
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; OTHER INFORMATION: n = a or c or US-09-880-107-3947
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LENGTH: 5086
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Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REPERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGram
SEQ ID NO 104
LENGTH: 4149
2864 GGACCCTCTGGTATTTCTGGCCCTCCTGGTCCCCTGGTCCTGCTGGGAAAGAAGGGCTT 2923
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                                              138 ProGlyProGln-------
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NAME/KEY: misc_feature
COTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.19
NAME/KEY: unsure
LOCATION: 1492-1495, 1663, 1669, 4012, 4055
COTHER INFORMATION: a, t, c, g, or other
US-10-044-090-104
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2426 GGCCCAGCTGGTCCAAATGGTCCCCCCGGTCCTGCAGGAGTCGTGGTGATGGAGGCCCC 2485
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Mismatches:
Indels:
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Matches:
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FILE REFERENCE: PAIO2
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/USO0/05883
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 1999-03-124,270
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; NAME/KEY: misc_feature
; LOCATION: (5143)
; CTHER INFORMATION: n equals a,t,g, or
US-09-925-299-206
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COTHER INFORMATION: n equals a,t,g, or maker: misc_eature

COCATION: (17)

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COCATION: (5126)

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COCATION: (5126)

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COCATION: (5143)

COTHER INFORMATION: n equals a,t,g, or use incomment in the misc_feature

COCHER INFORMATION: 05143)
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NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
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Best Local Similarity:
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Sequence 22, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT FILING NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2699 GCCAAAGGGCCTAAGGGTGAAAACGGTGTTGTTGGTCCCACAGGCCCCGTTGGAGGCTGT 2758
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                                                                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.13
US-10-044-090-22
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Mismatches:
Indels:
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Matches:
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Search completed: March 21, 2003, 12:32:28 Job time : 186.172 secs

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BE910803 601661855
BO674807 AGENCOURT
BE290299 601089246
BD955927 AGENCOURT
AL568743 AL568143
AW958053 EST370123
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BQ771366 UI-M-FT0-
BM676508 UI-E-EX0-
BM713891 UI-E-EX0-
BM713891 UI-E-EX0-
BM713891 UI-E-EX0-
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BM713891 UI-E-EX0-
AM379436 CM4-HT024
AM379436 CM4-HT024
AM37843000 ALS43000
AM3617069
BQ887163 AGENCOURT
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BB749743 BB749743
BM907108 AGENCOURT
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I
( bases 1 to 3305)
Strausberg,R.
Direct Submission
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                          Description
                                                                                                                                                                                                                                                                                                                          BC013626
BQ921102
BM905999
BQ222937
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BI456015
BE929813
BQ955616
BG681943
BI249235
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                                   SUMMARIES
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AL543000
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BQ887163
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TITLE
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KEYWORDS
SOURCE
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4899.781 Million cell updates/sec
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                                                         March 21, 2003, 08:08:41; Search time 1130.43 Seconds
         GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                         nucleic search, using frame_plus_p2n model
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1940
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Maximum Match 100%
Listing first 45 summaries
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603170460 RC3-GN004

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Mus muscu

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pgf2c.pk0 BB613976 602626481

RC3-GN004 AGENCOURT

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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
JOURNAL
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BQ713873
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                                                                                                                                                                                                                                                                                               be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WAP-TGF alpha model. 7 months
                                                                                                                                                                                                                 Contact: amg@bcm.tmc.edu
Gunzatne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                               clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: h Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
Submitted (05-JUN-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1296 ATGCAGCAAGACATGATGAGGTCAAAGTTAGACACTGAAGTGGCCAACTTATCAGTGGTT 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: MGC help desk Email: Gapbs. remail.nih.gov Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AlaGlyGluArgGlyProIleGlyProAlaGlyProProGlyGluArgGlyGlyLysGly 100
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Location/Qualifiers
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14
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                                                                                                                                                                                     Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                             Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="C57BL/6J"
/clone="IMAGE:2811487"
/tissue_type="Mammary tumor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV-SPORT6"
757 c 760 g 757 t
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/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
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BQ713873 861 bp mRNA linear EST 16-JUL-2002 AGENCOURT_8482828 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6306240
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Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi;
Buarayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E 1 (bases 1 to 861)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capapbs-remail.nih.gov.
Tissue Procurement: Susan L. Sullivan, PhD.
CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
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Sciurognathi; Muridae; Murinae; Mus
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2136 GACGGGTCACCTGTTGATTACAAAACTGGAAAGCTGGACAACCAGATAACTGGGGCAGT
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BQ713873
BQ713873.1 GI:21852772
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helleAsnThrArgGluGluGlnGlnTrp-Ile-LysLysGlnMetValGlyArgGluSe 263
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1061.00
87.76%
82.86%
54.69%
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Mammalia; Eutheria;
1 (bases 1 to 906)
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TITLE
JOURNAL
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KEYWORDS
SOURCE
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                                                 /organism="Mus musculus"
//organism="Musculus"
//organism="Laxon:10090"
//olone="ImAGE: 3006240"
//olone="InAGE: 3006240"
//olone=lib="NIH_MGC_129"
//olone=lib="NIH_MGC_129"
//olone=lorgan: olfactory epithelium; Vector:
pCMV-SPORT6.1.ccdb; Site_1: EcoRY; Site_2: Not1; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2. 2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
                                                                                                                                                                                                                                                                                                                                       GlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGlyLeu 164
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114
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Mismatches:
Indels:
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Matches:
             column:
http://image.llnl.gov
Plate: LLAM13721 row: n col
High quality sequence stop: 5
Location/Qualifiers
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1256.00
91.01%
85.77%
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906 bp mRNA linear EST 21-AUG-2001
603172765F1 NCI_CGAP_Mam5 Mus musculus CDNA clone IMAGE:5251888 5',
BI456109
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                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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203
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26
6
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                                                                                                                                                                                                                                                                                                                                                                     /_clone="IMAGE:5251888"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7" months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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668 bp' mRNA linear EST 15-JUL-2002 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6212672
                                              /clone="InAGES:296.292"
/clone=lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="l0 months, virgin"
/lab_host="Organ: mammary, Vector: pCMV-SPORT6; Site_1: SalI;
/lab_host="Onbli Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                        /strain="FVB/N"
/db_xref="taxon:10090"
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AGENCOURT 8035172 NIH_MGC
5', mRNA Sequence.
BQ674807 GI:21785641
                                                                                                                                                                                                                                   4.81e-58
1022.00
96.34%
92.67%
52.68%
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cal Similarity:
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Mus musculus cDNA clone IMAGE:3962292 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgabbs-rémail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MG clone distribution information can ifound through the I.M.A.G.E. Consortium/LLNL at:
http://imag.llnl.gov
                                                                 LeuGlnGlyProProGlyProArgGlyProArgGlyAspArgGlySerGlnGlyProPro
                                                                                                                                                                                    101 SerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLysProGln
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High quality sequence stop: 580.
Location/Qualifiers
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BE910803
BE910803.1 GI:10407765
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AUTHORS
TITLE
JOURNAL
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425

138

65

580 1177 7 7 0 0

Matches:

Length:

158

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288 LysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGluAsp 307
               363 AAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGCCATGGGCCAGGAGAAGAC
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house mouse.
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                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:1621672"
/clone_lib="NHH_MGC_102"
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/tlssue_type="epidermoid carcinoma, cell line"
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Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRIXAhoI sites using the
following 5' adaptor: GGCAGGAG(5). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."
                               168 ProGlyValProGlyMetProGlyProLysGlyProProGlyProProGlyProSerGly 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 AlaValValProLeuAlaLeuGlnAsnGluProThrProAlaProGluAspAsnGlyCys 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228 PheGluAspAlaLysLeuPheCysGluAspLysSerSerHisLeuValPheIleAsnThr 247
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601089246F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3484163 5', MENA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Clone distribution: MGC clone distribution information can infound through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLAW8516 row: k column: 12
High quality sequence stop: 551.
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/dev_stage="7 months"
/lab_host="DH10B"
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                      302 GGTTGCCAGGCTTGCCAGGGTG-CCAGGCATGCCTGGGCCTAAGGGACCACCTGGCCCTC 360
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
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GAGGGCCACAATTGGACCAGTCGGCCCTCCTGGAGAGCGTGGCAGCAAAGGATCCAAAGG 121
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Apencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13740 row: 1 column: 13
High quality sequence stop: 665.
                                                                                   roGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrProAlaProG
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/clone="INAGE:6313500"
/clone=lib="NIH_MGC_129"
/lab_host="DH10B (phage-resistant)"
/note="Organ: olfactory epithelium; Vector:
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pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Average insert size user Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."

269 c 258 g 169 t 1 others
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Conservative:
Mismatches:
Indels:
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AL568743
AL568743.1 GI:12923387
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Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-JUN-2000
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 552)
Hegde, P., Qi.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                            ммээвиээ
EST370123 MAGE resequences, MAGE Homo sapiens CDNA, mRNA sequence.
AW958053
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Contact: John Quackenbush

The Institute for Genomic Research

712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528

Fax: 301 838 0208
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149
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Mismatches:
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, M
/note="Vector: pBluescript5Km"
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                               418 GAAAAAGACAGGAGACAGYACTGTCATCTGCATTA 383
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Matches:
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Plate: 115
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                                                                                                                                                                                                                                                             pcMVSPORT 6 vector. Library was constructed by Life
Technologies. Contact: Feng Liang Life Technologies, a
division of Invitrogen 9800 Medical Center Drive Rockville
, Maryland 20850, USA Fax: (1) 301 610 8371 Email:
fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSODE005YH04"
/clone_lib=TrI=FL002_PL1"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pCMVSPORT 6; 1st strand
CDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-stranded cDNA was digested with Not
and cloned into the Not I and Eco RV sites of the
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BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.genoscope.cns.fr.
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1 (bases 1 to 967)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length CDDA libraries and normalization
Comblished (2001)
Contact: Genoscope
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A rakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.

Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Mutsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Muramatsu,M. and Hayashizaki,Y., et al. 2001)

Lupublished (2011)
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                                                                                                                                                                                                                                                                                             BB248064 RIKEN full-length enriched, 7 days neonate cerebellum Mus musculus cDNA clone A730023E20 3', mRNA sequence.
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Email: genome-res@gsc.riken.go.jp,
ORL:http://genome.gsc.riken.go.jp,
ORL:http://genome.gsc.riken.go.jp,
Carninci, P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
agi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
Free Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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                                                                          361 ATTTATGCTGGGCAGGGGAACGATTTCCAATGTGAAGACGTCAATAACTTTAATTTGCGA 420
                   IleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspValAsnAsnPhe-IleCysGl
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Contact: Yoshihide Hayashizaki
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Computer-based methods for the mouse full-length CDNA
                                                                                                                             331 uLysAspArgGluThrValLeuSerSerAlaLeu 342
                                                                                                                                                             421 AAAAGACAGGAGACAGTACTGCATTA 454
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/organism="Mus musculus"

.638

source

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3'j. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
/clone="A730023E20"
/clone_lib="RIKEN full-length enriched, 7 days neonate
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Mismatches:
                                                                                                                                                                                                                                                                                                                            146 t
                                       /tissue_type="cerebellum"
/dev_stage="7 days neonate"
/lab_host="DH108"
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BQ891432 936 bp mRNA linear EST 16-AUG-2002 AGENCOURT_8754195 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6332754
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10090"
/clone="IMAGE:6332754"
/clone="IMAGE:6332754"
/clone="Lib-"NIH_MGC_130"
/lab_host="H10B (phage-resistant)"
/note="Organ: otocysts; Vector: pCMV.SPORT6.1.ccdb;
Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 936)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy L. Freeman,
                                                                                                       LeuPheCysGluAspLysSerSerHisLeuValPheIleAsnThrArgGluGluGlnGln 252
                                                                                                                                                                                                                                                                              242 CAGGAAAGCGAATGGAAGTGGCTAGACGGGTCACTGTTGATTACAAAAACTGGAAAGCT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                            313 TyralaglyGlnTrpAsnAspPheGlnCysGluAspValAsnAsnPheIleCysGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ph.D. cDNA Library Preparation: ResGen, Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MCC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13790 row: n column: 19
High quality sequence start: 25
High quality sequence storp: 632.
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1. .936
/organism="Mus musculus"
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BQ891432
BQ891432.1 GI:22283446
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I (Dases 1 to 808)

INIH-WCO http://mgc.nci.nih.gov/.

INIH-MCO http://mgc.nci.nih.gov/.

Inpublished (1999)

L Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution in the Contact in MCC clone distribution in the Contact in MCC clone distribution in the Contact in MCC clone distribution in information can be
           BQ771366 808 bp mRNA linear EST 26-JUL-2002
UI-M-FIO-byu-g-09-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone
IMAGE:5702432 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone was contributed by the Brain Molecular Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AlaLeuGlnAsnGluProThrProAlaProGluAspAsnGlyCysProProHisTrpLys 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
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/strain="C57BL/6"
/db_xref="taxon:10090"
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                                                                                                             BQ771366
BQ771366.1 GI:21979842
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767.00
93.33%
87.33%
39.54%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo saplens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 500)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                    81 AlaGlyGluArgGlyProIleGlyProAlaGlyProProGlyGluArgGlyGlyLySGly 100
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                                                                                             1 MetGlnGlnAspLeuMetArgSerArgLeuAspThrGluValAlaAsnLeuSerValIle 20
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                                                            US-09-763-712A-2_COPY_206_547 (1-342) x BQ891432 (1-936)
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Mismatches:
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Location/Qualifiers

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source

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FEATURES

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Chorotoe="fetal and adult"

//lab_host="DH10B (Life Technologies) (T1 phage resistant)"

//lab_host="DH10B (Life Technologies) (T1 phage resistant)"

//note="Organ: eye; Vector: pT73 Pac (Pharmacia) with a
modified polylinker; Site_1: ECON I: Site_2: Not I:
UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an ECON I adaptor, digested
with Not I, and cloned directionally into PT73-Pac
vector: The oligonucleotide used to prime the synthesis of
first-strand cDNA contenins a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA;
lloss CGATTAGGCA; eye anterior sequence, AGAATCAAGA;
lloss CGATTAGGCA; eye anterior sequence, This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-EJO
TAG_LIB=UI-E-EJO
TAG_SEO=AATGCCGCAT;
OP a 123 c 89 9 179 t
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                                        /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and
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Conservative:
Mismatches:
Indels:
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UI-E-EJC-ahq-c-05-0-UI.rl UI-E-EJO Homo s
UI-E-EJO-ahq-c-05-0-UI 5', mRNA sequence.
BM713891 GI:19027149
/clone="UI-E-EJO-ahq-c-05-0-UI"
/clone_lib="UI-E-EJO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
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669.00
100.00%
99.15%
34.48%
                                                                                 Choroid"
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Best Local Similarity:
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In Chases I to 591)

IN Clases I to 591)

IN Class I to 591)

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.ih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: Sanopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: Info@image.llnl.gov

High quality sequence stop: 441.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              dai33d10.y2 NICHD XGC Sp1 bp mRNA linear EST 21-AUG-2001 dai33d10.y2 NICHD XGC Sp1 Xenopus laevis cDNA clone IMAGE:4963626 5' similar to SW:LECH_RAT P02706 ASIALOGLYCOPROTEIN RECEPTOR 1;, BI445884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Organism="Xenopus laevis"
/Ob_xref="taxon:8355"
/Clone="IMAGE:4958626"
/Clone=lib="NICHD KGC Spl"
/Gev_stage="adult"
/Ab_host="phi08" (phage-resistant)"
/note="organ: spleen; Vector: pCMV-SPORT6; Site_1: Not1:
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
#Aperage insert size 2.4 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                     286
                                                                                           287 TyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGlu 306
                                                                                                                                                                                                                                                           307 AspCysAlaGlyLeuIleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspValAsn 326
                                                                                                                                                                                                                                                                                    243 GACTGTGCGTTGATTTATGCTGGGCAGTGGAACGATTTCCAATGTGAAGACGTCAAT 302
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                                                                                                                                                                                        183 TACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGCCATGGCCAGGAGAA
                                                                       GlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGlyThrSerProAsp
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118 c
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BI445884
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AUTHORS
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/dev_stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT773-pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted CDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand CDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (TT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAGA; lens, CGATTAGCGA; eye anterior segment, AATGCCGAT; optic nerve, CCATTAAGTG; retina, CCGCG; Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                              Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 443-498, >POLY_A#Simple_repeat
                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UI-B-EJO-ahq-c-05-0-UI"
/clone=lib="UI-B-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
optic nerve, retina, Retina Foveal and Macular, RPE and
                                                                                                            1 (bases 1 to 507)

Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                    Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 ThrArgGluGluGlnGlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrpIle 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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218
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                                                                                                                                                                                                               165 -----ProGlyLeuProGlyValProGlyMetProGlyProLysGlyProProGlyPro 182
                                                                  204
                                                                                183 ProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrPro---- 200
                                                                                         146 PheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGlyLeu--- 164
-----AlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAspLysCys
                                                            145 GGACCTCCAGGAATACCTGGATTACCTGGAATACCTGGACCTAGAGGTCCTCCAGGGCCT
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Human secreted pro
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Nucleotide sequenc
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Bovine alphal(III)
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-MODEL=frame+pan.model -DEV=xlp
-DE-XGD02_1/USPTO_spool/US09763712/runat_14032003_100949_18091/app_query.fasta_1.1877
-DB-N_Geneseq_101002 -OFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=-0 -UNITS-bits -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGN=200 -THR-SCORE=-DECT -THR_MAX_100 -THR_MIN-0 -ALIGN=15
-MODE-LCCAL -OUTFNT=pto -NORM-ext -HEAPSIZE=500 -MINLEN-0 -MAX.EN=200000000
-USER=US09763712_eCGN_1 1_656_erunat_14032003_100949_18091 -NCPU=6 -ICPU=3
-NO_XEPX* -NO_MANP -LARGEQUER* -NEC_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Title: Perfect score:

Sequence:

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Run on:

Scoring table:

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AlaAsnGluGlnAsnLeuLysAspLeuGlnAspLeuHisLysAspAlaGluAsnArgThr 

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AsnAsnThrLeuAlaAsnIleArgLeuAspSerValSerLeuArgMetGlnGlnAspLeu 

GluValArgThrThrCysThrAspThrLeuThrLysHisThrAspAspLeuThrSerLeu

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804

141 745 805

161

865 201 925

181

LysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGly 

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ProlleGlyProAlaGlyProProGlyGluArgGlyGlyLysGlySerLysGlySerGln 

984

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The invention relates to polynucleotides encoding a new collectin of human origin. The collectin can be used as an antibacterial and antiviral agent and for screening potential drug molecules. The new collectin can be produced by standard recombinant methodology. The present sequence
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                  TTCCAGGGACTTCAGGGCACCGTTGGGGAGCCTGGGGTGCCTGGACCTCGGGGACTGCCA
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                                                                                                                                                                                                                                 Human; scavenger; receptor; diagnosis; treatment; autoimmune disease; rheumatoid arthritis; gene; ss.
          lleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGlyThrSerPro
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arteriosclerosis; diabetes; bacterial infection; restenosis; angloplasty;
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                                                                                                                                                                                                         2009 AACACTAGAGAGGAACAGCAATGGATAAAAAAACGGAGGTGGTAGGGAGGAGCCACTGG
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Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM3642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and
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The present invention provides the protein and coding sequences for 25 novel extracellular matrix and adhesion-associated proteins (EXMADS). These are designated EXMAD-1, EXMAD-3, EXMAD-3, EXMAD-5, EXMAD-6, EXMAD-1, EXMAD-10, EXMAD-11, EXMAD-11, EXMAD-12, EXMAD-13, EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-19, EXMAD-23, EXMAD-24, and EXMAD-19, expand-14, EXMAD-17, EXMAD-18, EXMAD-19, are useful in the prevention and treatment of cancers, cell proliferation, cardiovascular, reproductive, immune, musculoskeletal, developmental and
                                                                                                                                                                                                                                     treating, or
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11-MAY-1999,
23-AUG-1999,
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                                                                                                               Azimzai
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1287 ccaggcccccccggcccaccaggcaaagagggacrccccggccrccagggcccrccrggc 1346
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GAAATTTTTGAGGATGCAAAGCTTTTCTGTGAAGACAAGTCTTCACACATCTTTGATA
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                                     LysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGly
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protein;
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immunostimulant; antiparasitic; secreted protein; transmembrane protein; cytokine; cell proliferation; cell differentiation; autoimmune disease; stem cell; growth factor; nervous system disease; neuropathy; Alzheimer's disease; Parkinson's disease; Huntington's disease; osteoporosis; severe combined immunodeficiency; SCID; infection; multiple sclerosis; rheumatoid arthritis; gene therapy; gene; ss.
                                                                                                                                                                                                                                    Evans C;
                                                                                                                                                                                                                                    Collins-Racie LA,
                                                                                                                                                                                                                                                                                                                                   Claim 250; Page 231-232; 284pp; English.
                                                                                                                                                                                                                                    LaVallie ER,
Spaulding V;
                                                                                                                  22-DEC-2000; 2000US-0745763;
                                                                                                                                    98US-0040963
                                                                                                                                                             MCCOY J M.
LAVALLIE E R.
COLLINS-RACIE I
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                                                                                                                                                                                         EVANS C.
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                                                                               JS2002065394-A1.
                                                                                                                                                                                                MERBERG
                                                              Homo sapiens.
                                                                                                                                    18-MAR-1998;
                                                                                                30-MAY-2002.
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Merberg D,
                                                                                                                                                                                                          (TREA/)
(SPAU/)
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(COLL/)
(EVAN/)
(MERB/)
                                                                                                                                                                                                                                              Merberg
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The invention relates to human secreted or transmembrane protein (1), their fragments and is encoded by specific complementary deoxyribonucleic acid (CDRA) inserts (11), where the protein is substantially free from other mammalian proteins. (1) are useful for preventing, treating or meliorating a medical condition, especially immunological treatment or prevention of tumours. (1) exhibits activity relating to angiogenesis, cytokine, cell proliferation, cell differentiation, antilnflammatory, stem cell growth factor activity and activity or inhibin-related activities. (1) can be used to manipulate stem cells in culture to give rise to neuroepithelial cells that can be used to augment or replace cells damaged by illness, autoimmune disease, accidental damage or regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic activity, regulation of haematopolesis and is useful for treating myeloid or lateral sclerosis. (1) is involved in chemotactic or chemokinetic activity, regulation of home, cartilage, tendon, ligament and/or nerve (1) sainolated disorders such as thrombocytopaenia cativity, regulation of home, cartilage, tendon, ligament and/or nerve (1) sainolated disorders such as thrombocytopaenia con for regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including cepeneration and treatment of lung or liver fibrosis, reperfusion injury and anterious immune deficiencies and disorders including cepeneration and encoder or produced immuned deficiencies and disorders including cepeneration and encoder or produced immune deficiencies and disorders including cepeneration and preatment of lung or liver fibrosis, reperfusion injury and an encoder or produced immuned deficiencies and encoders including anterior and preatment of an encoder or produced in various fibrosis. autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. (II) is useful to express recombinant protein, as markers for tissues in which the corresponding protein is preferentially expressed and in gene therapy. The present sequence is that of a polynucleotide of the invention

Sequence 2929 BP; 901 A; 699 C; 692 G; 637 T; 0 other;

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                                                            (1-2929)
      Length:
Matches:
Conservative:
Mismatches:
                                                            x ABQ92072
                                     Indels:
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                                                           US-09-763-712A-2_COPY_91_547 (1-457)
      3.74e-80
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Alignment Scores:
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Secreted protein; human; nutritional supplements; immune stimulant; immune suppressor; haematopolesis regulator; tissue growth; chemotaxis; activin/inhibin; chemokinesis; haemostasis; thrombolysis;
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AsnThrargGluGluGluGlnGlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrp
                                                                                   GluAspCysAlaGlyLeuIleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspVal
                                                                                                                                                                                                                                                                                                                                             receptor/ligand activity; anti-inflammatory; tumour inhibitor; cadherin/tumour invasion suppressor; ds.
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                                                                                                                                                                                                                                                                                                     bv227_1 coding sequence.
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Treacy M;
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V,
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                                                                                                                                                                                                                                                     standard; cDNA; 2930
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97US-0868696.
97US-0868697.
97US-0868898.
97US-0868899.
97US-0868199.
97US-086819191.
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97US-0869194
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04-JUN-1997;
04-JUN-1997;
04-JUN-1997;
04-JUN-1997;
04-JUN-1997;
04-JUN-1997;
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04-JUN-1997;
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McCoy JM,
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This sequence encodes a human secreted protein of the invention.
This DNA sequence was isolated from a human adult brain cDNA
library, and was designated clone bv227_1. The DNAs and proteins
are predicted to have biological activities which would make them
suitable for treating, preventing or ameliorating medical conditions in
humans and animals, although no supporting data is given. Suggested
activities include nutritional sources or supplements, immune
stimulating or suppressing activity, haematopoissis regulating activity,
tissue growth activity, activin/inhibin activity,
chemotactic/chemokinetic activity, haemostatic and thrombolytic activity,
chechtor/ligand activity, anti-inflammatory activity, cacherin/tumour
invasion suppressor activity, and tmour inhibition activity. The DNAs
are also stated to be useful for gene therapy. A host cell transfected
with the DNA, or its subfragments and variants is useful for recombinant
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                                                              derived from
                                                            New polynucleotides encoding secreted human proteins - derived from human foetal brain, adult brain, foetal kidney, adult ovary, adult retina, adult placenta or adult uterus cDNA libraries
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Matches:
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                                                                                                                        26; Page 87-88; 127pp; English
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                                                           New polynucleotides
human foetal brain.
              WPI; 1999-059912/05.
P-PSDB; AAW73628.
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GlyProLysGlySerArgGlySerProGlyLysProGlnGlyProGlnGlyProSerGlyAsp
                                                                                                             1581 GGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGTGGGGAC
                                                                                                                                                                                PheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGlyLeuPro
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                                                                                                                                    ProGlyProProGlyProProGlyLysGluGlyLeuProGlyProGlnGlyProProGly
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                nGluValArgThrThrCysThrAspThrLeuThrLysHisThrAspAspLeuThrSerLe
                                                                   uAsnAsnThrLeuAlaAsnIleArgLeuAspSerValSerLeuArgMetGlnGlnAspLe
                                                                                                                             sLeuValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProPr
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Note: The sequence data for this patent did not form part of the printed
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Conservative:
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Indels:
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Xu C, Xue AJ,
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Wang Z, Wehrman T, Xi
Zhou P, Goodrich R,
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25-APR-2000; 2000US-0552317.
9-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0662191.
19-CT-2000; 2000US-0693036.
29-NOV-2000; 2000US-059344.
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Best Local Similarity:
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                                      WO200153312-A1
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disorder;
Human; angiogenesis; PRO protein; cardiovascularisation; wound; atherosclerosis; cardiac hypertrophy; gene therapy; endothelial cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; gene; ss.
                            1637 CAATAACTTCATTTGCGAAAAAGACAGGAGACAGTACTGTCATCTGCATTA 1688
                      440 lAsnAsnPheIleCysGluLysAspArgGluThrValLeuSerSerAlaLeu
                                                                                                           Human angiogenesis related cDNA PRO7223 SEQ ID NO: 27
                                                                ABL95574 standard; cDNA; 2005
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2000WO-US32678.
2000US-0747259.
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2001WO-US06520.
2001WO-US06666.
2001US-0802706.
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2001US-0767609.
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2000WO-US30952
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2001US-0870574
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2001WO-US00000
                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FERR/) FERRARA N.
(GERB/) GERBER H.
(GERR/) GERRITSEN M E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENENTECH INC
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FERRARA N.
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15-SEP-2000;
18-SEP-2000;
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09-MAR-2001;
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01-DEC-2000;
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24-OCT-2000;
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08-NOV-2000;
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                                                                               ABL95574;
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosting a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, may candial infarctions, thrombophiebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The present sequence is a coding sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal
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Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J,
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2005 BP; 606 A; 493 C; 491 G; 415 T; 0 other;
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             GODOWSKI P J.
GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                  PAN J.
PAONI N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
                                                                                                                                                                                                                                                                                                                                                WPI; 2002-171999/22.
GODDARD A.
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Best Local Similarity:
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PRO7223 cDNA sequence SEQ ID NO:27

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           CTAGTAGACTCCAAGCATGGTCAGCTCATCAAGAATTTTACAATACTACAAGGTCCACCG
                      ProlleGlyProAlaGlyProProGlyGluArgGlyGlyLysGlySerLysGlySerGln
                                                                 GlyProLysGlySerArgGlySerProGlyLysProGlyProGlnGlyProSerGlyAsp
                                                                      SerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrProAlaProGluAspAsn
                                                                                                                                                              GlullePheGluAspAlaLysLeuPheCysGluAspLysSerSerHisLeuValPheIle
                  GlyProArgGlyProArgGlyAspArgGlySerGlnGlyProProGlyProThrGlyAsn
                                  LysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGly
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Human; anglogenesis; cardiant; cytostatic; antianglogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; anglogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; anglna; hybematoid arthritis; mycoardial infarction; thromophlebitis; lymphangitis; tumour anglogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mapping; gene mapping; gene; ss.
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L, Hillan KJ, Marsters SA, Pan J,
EK, Williams PM, Wood WI, Ye W;
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20000S-219556P.
20000S-22064P.
20000S-220664P.
20000S-022695P.
20000S-023328.
20000S-023328.
20000S-230978P.
20000S-230978P.
20000S-230978P.
20000S-242922P.
20000S-064610.
20000S-0709238.
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20000S-0739238.
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2001WO-US17800
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Watanabe CK,
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P-PSDB; ABB84830.
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28-JUL-2000;
07-AUG-2000;
17-AUG-2000;
24-AUG-2000;
18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
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28-FEB-2001;
01-MAR-2001;
09-MAR-2001;
14-MAR-2001;
22-MAR-2001;
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01-DEC-2000;
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10-MAY-2001;
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activities, and can be used in gene therapy. The PRO polynucleotides, proteins, agonists and antagonists are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-related macular degeneration, therosoclerosis, hypertension, arterial restenosis, rheumatoid arthritis, angina, mycoardial infarctions, thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast carcinoma and liver carcinoma) and wound healing. The PRO polynucleotides have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. ABLB81259 to ABLB81267 represent primers and probes used in the exemplification of the present invention.
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Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angloplasty;
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                                                                           AsnThrargGluGluGlnGlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrp 380
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                           GluAspCysAlaGlyLeuIleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspVal
                     PheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGlyLeuPro
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                                                                     New Scavenger receptor proteins SRCL-P1 with collectin-like structure, useful for treatment and diagnosis of diseases associated with oxidized low-density lipoprotein accumulation
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Mismatches:
Indels:
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Matches:
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Query Match:
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Human; scavenger receptor; SRCL-P1; macrophage; basal immunity;
arteriosclerosis; diabetes; bacterial infection; restenosis; angioplasty;
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                          GlyProArgGlyProArgGlyAspArgGlySerGlnGlyProProGlyProThrGlyAsn
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                                                                                                                                                                                                           New Scavenger receptor proteins SRCL-P1 with collectin-like structure, useful for treatment and diagnosis of diseases associated with oxidized low-density lipoprotein accumulation
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Matches:
Conservative:
Mismatches:
Indels:
/product= "scavenger receptor"
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1738.00
72.87%
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2000JP-0309068
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P-PSDB; AAG63350.
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Best Local Similarity:
                      WO200159107-A1
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10-OCT-2000;
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving to restore normal activity of (II) or to treat disease states involving quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical clasorders involving aberrant protein esquences have applications in the printed diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of data and products dependent on DNA and diagnostic coding sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                     forensic;
                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1521 BP; 386 A; 420 C; 425 G; 290 T; 0 other;
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DNA encoding novel human diagnostic protein #6937
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Best Local Similarity:
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Cellular stress response protein; CSR1; CSR2; CSR3; human; macrophage; scavenger receptor protein; intracellular stress; arteriosclerosis; diabetic circulatory obstruction; microbial infection; ss.
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LysGlyProProGlyProProGlyProSerGlyAlaValValProLeuAlaLeuGlnAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277 CCACCTGGCCCTGCGGGTGAGAGAGCCCCAATTGGACCAGCTGGTCCCCCCGGAGAGGT
                                                                                                                                                        LeuProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluPro
                                                                                                                                                                                                                                                                                                                                                                                            AspLysSerSerHisLeuValPheIleAsnThrArgGluGluGlnGlnTrpIleLysLys
                                                                                                                                    212 GlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLys
                                                                                                                                                                                                                                                                                                                 GlyValProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGGGCCCCCCCGGCCCTCCTGGCCCATCAGGAGCGGTGGTGCCCCTGGCCCTGCCAGAAT
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                                                           ProproGlyProAlaGlyGluArgGlyProIleGlyProAlaGlyProProGlyGluArg
                                                                                                                                                                                                                   ProGlyProGlnGlyProSerGlyAspProGlyProProGlyProProGlyLysGluGly
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This sequence encodes the human cellular stress response 1 (CSR1) protein of the invention. The CSR proteins are macrophage scavenger receptor proteins. The CSR proteins can be used in the treatment, gene therapy and diagnosis of diseases in which intracellular stress is important, such as arteriosclerosis, diabetic circulatory obstruction, and microbial infection. Expression of the proteins is induced in vivo in response to
                                                                                                                                 1618 GCCCCCTGGGACCCCAGGGTCCTCAGGGCGAACCTGGAGAGGCCGGGCCTGTGGGAAA 1677
                                                                                                                                                                                                                                                                                        1840 CCGGGAATTGCAGGGAAGACAGGGTCACCAGGCCAGCGGGGGCCATGGGGCCTAAGGGT 1899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cellular stress response protein; CSR1; CSR2; CSR3; human; macrophage; scavenger receptor protein; intracellular stress; arteriosclerosis; diabetic circulatory obstruction; microbial infection; ss.
                                                      1678 AGGGGCCCTGTTGGCCCTCGAGGCTTCCCAGGCCTCAAAGGCTCAAAGGCCAGCTTTGGA 1737
1498 CGCAATGTCACCATCCTACGAGGTGCCCCCGGCCCTCCAGGACCAAGAGGATTCAAAGGA 1557
                                                                                                                                                                                        ArgGlyProlleGlyProAlaGlyProProGlyGluArgGlyGlyLysGlySerLysGly 218
                                                                                                                                                                                                                                                                 SerGlnGlyProLysGlySerArgGlySerProGlyLysProGlyProGlnGlyProSer 238
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                                                                                                             .-----LysGlyGluProGlyProProGlyProAlaGlyGlu 198
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                                     SerGlnGlyProProGlyProThrGlyAsnLysGlyGlnLysGlyGlu-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CSR1 protein coding sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence encodes the human cellular stress response 3 (CSR3) protein of the invention. The CSR proteins are macrophage scavenger receptor proteins. The CSR proteins can be used in the treatment, gene therapy and diagnosis of diseases in which intracellular stress is important, such as arteriosclerosis, diabetic circulatory obstruction, and microbial infection. Expression of the proteins is induced in vivo in response to intracellular stress, and inhibits cell death as a result of such stress.
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                                                                                                                                                                                                                                                                                                                                  Scavenger receptor proteins - for treatment and diagnosis of disorders involving cell stress
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Conservative:
Mismatches:
Indels:
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682.00
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                                                                                                                                                                                                        (NISB ) JAPAN TOBACCO INC.
                                                                                                                                                                                                                                         Nakamura Y, Tokino T;
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Best Local Similarity:
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Homo sapiens.
                                 WO9909159-A1
                                                                                                                                                                 13-AUG-1997;
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                       Sequence 3810 BP; 892 A; 1213 C; 1049 G; 655 T; 1 other;
                                                                                                                                                          US-09-763-712A-2_COPY_91_547 (1-457) x AAX27856 (1-3810)
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Matches:
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Search completed: March 21, 2003, 08:38:02 Job time : 262.038 secs Appl Appli Appli

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APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-4187

CMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                   US-09-484-970B-4
US-09-029-348-20
US-08-249-200-5
US-08-494-10-5
US-09-497-206-40
US-09-457-702B-264
US-09-457-702B-264
US-09-457-702B-62
US-08-393-367B-1
US-08-393-367B-1
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US-08-393-367B-1
US-08-999-336-1
US-09-911-470-3
US-09-111-470-3
US-09-111-470-3
US-09-453-702B-65
US-09-453-702B-67
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ATTORNEY_AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: 45556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 494-8700
TELEFAX: (415) 494-8701
TELEFAX: 910 277299 FHT UR
INFORMATION FOR SED ID NO: 60:
SEQUENCE CHARACTERISTICS:
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California
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2886.622 Million cell updates/sec
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                                                                                                                                    March 21, 2003, 08:26:21; Search time 48.552 Seconds
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   /cgn2_6/ptodatcal/ina/5B_COMB.seq:*
3: /cgn2_6/ptodatcal/ina/6A_COMB.seq:*
4: /cgn2_6/ptodatcal/ina/6B_COMB.seq:*
5: /cgn2_6/ptodatcal/ina/pcruC_COMB.seq:*
6: /cgn2_6/ptodatcal/ina/pcruC_COMB.seq:*
            GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                            OM protein - nucleic search, using frame_plus_p2n model
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US-09-029-348-19
US-08-159-784-1
US-09-297-269-39
US-08-555-669-11
US-09-073-663-11
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US-08-655-086-1
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-08-642-255-48
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       412 CGTGGCGATCCGGGACCACCGGGTGCACCTGGCCCAGCGGGTCCGCCTGGATCTAGAGGT
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                                                                                                                                                                                   Conservative:
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Indels:
                                                                                                                                                  Length:
Matches:
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Patent No. 5821089
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GRUSKIN, ELLIOTT A.
APPLICANT: ZHANG, GUANGHUI
APPLICANT: ZHANG, GUANGHUI
APPLICANT: CONNOLLY, KEVIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: DILWORTH & BARRESE
STREET: 333 BARLE OVINGTON BOULEVARD
CITY: UNIONDALE
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 -----AlaProGluAspAsnGlyCysPro 323
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                                                     , ...our.culb TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic"
US-08-642-255-60
                                                                                                                                         3.53e-18
459.50
53.16%
48.95%
18.23%
810 base pairs
            nucleic acid
EDNESS: double
                                                  linear
                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
               TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: line
                                                                                                                                  Alignment Scores:
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No.:
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1013 CCTGGCGCAGATGGTGTTGCTGGTCCCAAGGGTCCCGCTGGTGAACGTGGTTCTCCTGGC 1072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 LeuGlnGlyProProGlyProArgGlyProArgGlyAspArgGlySerGlnGlyProPro 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1073 CCCGCTGGCCCCAAAGGATCTCCTGGTGAAGCTGGTCGTCCCGGTGAAGCTGGTCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 --------GlyPheGlnGlyLeuGlnGlyThrValGlyGluPro
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                                                                         Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                        APPLICATION NUMBER: US/08/655,086 FILING DATE: 03-JUN-1996 CLASSIFICATION: 435
                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: STEEN, JEFFREY S.
REGISTRATION NUMBER: 32,063
REFERENCE/DOCKET NUMBER: 203-TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-228-8484
                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.58e-17
452.50
52.118
46.48%
17.96%
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                          LENGTH: 3181 base pairs
TYPE: nucleic acid
                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                  516-228-8516
                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                 unknown
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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580 CCTGCAGGCCCGCCAGGTGCGCCTGGTCCACCGGGTGCTCCGGGACCTGCA 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 LeuProGlyValProGlyMetProGlyProLysGlyProProGlyProProGlyProSer 301
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                        165 ProArgGlyAspArgGlySerGlnGlyProProGlyProThrGlyAsnLySGlyGlnLys 184
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                                                                                                                                                                                              220 GCGCCTGGACCGGCTGGTCCACCGGGTGCTCCGGGACCTGCAGGCCCGCCAGGTGCGCCT
                                                                                                            185 GlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGlyProIleGlyPro
                                                                                                                                       225 SerArgGlySerPro-----GlyLysProGlyProGlnGlyProSerGlyAspPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-763-712A-2_COPY_91_547 (1-457) x US-09-029-348-19 (1-1608)
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102
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67
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: THE VICTORIA UNIVERSITY OF MANC
TITLE OF INVENTION: NOVEL PROCOLLAGENS
FILE REFERENCE: d087857PUS LISTING
CURRENT APPLICATION NUMBER: US/09/029,348
CURRENT FILING DATE: 1998-05-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PALENTIN VGT: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 19, Application US/09029348 Patent No. 6171827 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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47.06%
40.00%
17.32%
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OTHER INFORMATION:
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
US-09-029-348-19
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                                           1424 GAACAAGGCCCTGCTGCTCCCCC---GGATTCCAGGGTCTCCCTGGTCTTGCTGGTCCT 1480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 LeuAspThrGluValAlaAsnLeuSerValIleMetGluGluMetLysLeuValAspSer 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 CTGGACCGGCTGGTCCACCGG - - - - - GTGCTCCGGGACCTGCAGGCCCGCCAGGTG 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 LysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProProGlyProArgGly 164
  -----AlaValValProLeuAlaLeuGlnAsnGluProThrProAla----
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                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: CAPPELLO, Joseph
APPLICANT: CAPPELLO, Joseph
APPLICANT: FERRARI, FRANCO A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
TITLE OF INVENTION: Protein Polymers
NUMBER OF SEQUENCES: 135
CORRESPONDENCES: 135
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
                                                                                                                          1481 CCAGGTGAAGCAGGCAAACCTGGTGAACAGGGTGTTCCT 1519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches:
Conservative:
Mismatches:
Indels:
                                                                                      -------323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LECULE TYPE: other nucleic acid DESCRIPTION: /desc = "synthetic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                  Sequence 50, Application US/08642255
Patent No. 5773249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bettram I.
REGISTRATION NUMBER: 20,015
REFRENCE/DOCKET NUMBER: A5555
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8770
TELERS: 910 277299 FFT URLERS: 910 277299 FFT URLERS: 910 27729
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448.50
52.70%
44.59%
17.80%
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LENGTH: 756 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
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US-08-642-255-50
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303
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                                                                                                                                                                                                                                          417
                                                                                                                                                                                                                                                                                                                                       718 CCTGGTACGGTTGGACCTGCTGG-CATTCGAGGCCCTCAGGGTCACCAAGGCCC----- 770
-----AlaGlyGluArgGlyProIleGlyProAla 205
                                                                                                                                                     GlyProProGlyGluArgGlyGlyLysGlySerLysGlySerGlnGlyProLysGlySer 225
                                                                                                                                                                        237
                                                                                                                                                                                                                                                                                             418 CCTGCTGGCAAACATGGAAACCGTGGTGAAACTGGTCCTTCTGGTCCTGTTGGTCCTGCT 477
                                                                                                                                                                                                                                                                                                                         251 GlyLeuProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGlu 270
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                                        185 GlyGluLysGlyGluProGlyProProGlyPro-----
                                                        238 CAGTATGATGGAAAAGGAGTTGGACTTGGCCCTGGACCAATGGGCTTAATGGGACCTAGA
                                                                                                                                                                                                                          226 ArgGlySerProGlyLys-------ProGlyProGlnGlyPro-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     658 GGTCCTAGGGGCCCTGCTGGTCCTTCTGGCCCTGGAAAAAAAGATGGTCGCACTGGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 Cys---ProPro-----HisTrpLysAsnPheThrAspLysCys 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08159784
Patent No. 5643783
GENERAL INFORMATION:
APPLICANT: BJorn R. Olsen
TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
STATE: Massachusetts
COUNTR: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOSTWARE: WORDERFIECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           293 GlyProProGlyProProGlyProSerGly-----
                                                                                                                                                                                                                                                                                                                                                                              271 ProGlyValProGlyProArgGlyLeuPro-----
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-159-784-1
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1087 CCTGGTGAAGATGGGAGACCGGTGACACTGGACCTCAAGGCTTTCCAGGGACCCCCAGGA 1146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 AlaGlyPro---------ProGlyGluArgGlyGlyLysGlySerLysGly 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 LeuValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProPro 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     166 ------ArgGlyAspArgGlySerGlnGlyProProGlyProThrGly 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArg--- 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SerGlnGlyProLysGlySerArgGlySerProGlyLysProGlyProGlnGlyProSer
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                                                                                                                                                                                                                                                                                                                           4031
95
15
49
78
                                                                                                                                                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
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                                                            00246/170001
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                                   REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-8906
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                   1.07e-15
428.00
46.41%
40.08%
16.98%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyProArgGlyPro-----
ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
                                                                                                                 TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          LENGTH: 4031
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-159-784-1
                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                 Pred. No.:
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0y 273 ValProGlyPro	RECISTRATION UNDER: 22,22/ REFERENCE/DOCKET NUMBER: 48389-030 TELECOMMUNICATION INFORMATION: TELEPAX: 415-854-3660 TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 2543 base pairs TYPE: nucleic acid
PERSONT	473 GUIGITGATCAAGGGCTTCTCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTCAAGGTTCTAAGATTGAAGATTGAAGATTGAAAGAATTTTTAAAGAATTTTAAAAAA

Qy Db 1	0 do	I QQ	Qy Db 1	QY Db 1	Qy Db 2	RESULT US-09- ; Sequ	GEN	+ <b>z</b> o					« 		NI	·· ·· ··		· · ·	-60-sn ; ;	
			2roGly 161         CGGGA 1030	AsnLys 181      SAGAAG 1090	31yPro 201 			AGARG 1270 31yPro 243 11 1				SGTGTT 1510	roGly 287         crGGC 1570	288		CTTTG 1690				3666AG 1810
	Length: 2543 Matches: 121 Conservative: 26 Mismatches: 91 Indels: 9	US-08-555-669-11 (1-2543)	ysAsnPheThrIleLeuGlnGlyProProGly ::	erGlnGlyProProGlyProThrGlyP 	lyProProGlyProAlaGlyGluarg( 	rgGlyGlyLysGlySerLysGlySer-       scGGTGAGGCTGGCCACCGGGGCTCN	GlnGlyProLys	CCCCCAGGCCTCCAGGCCTCCAGGGCCCCCAGGCCCCCAGGCCCCCAGGGCCAGGTGAGGAG	roGlyProGlnGlyProProGlyPheC 	CAGCGGCTGGTCGGACCCAAAGGAC		SCACCCAGGGTCCCAACGGCACCAGCC	rgGlyLeuProGlyLeuProGlyValE         GGGCTGCAGGGCGTCCCGGGTGTTC		aggaggccagcgagcgcatcaggc	ACAGTTAGCCGCGCACCTAAGGAAGC	-ProGlyProLysGlyProProGlyProProSer		AsnGluPro	3ACCCCCGGATACCGCGGTCCCAC16
STRANDEDNESS: unknown TOPOLOGY: unknown MOLECULE TYPE: cDNA FRATURE: RAME/KEY: CDS LOCATION: 472098	cores: 2.11e-15 419.00 1larity: 35.59 Similarity: 29.30% 16.63%	-763-712A-2_COPY_91_547 (1-457) x	ValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProPr :::    :::    :::        CTCGATGGCCAGAAGGAGGCTGGTCGCAACGGTGCTCC	ProArgGlyProArgGlyAspArgGlySerGlnGlyProProGlyProThrGlyAsnLyS :::	GlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGlyPro    ::::::	IleGlyProAlaGlyProProGlyGluArgGlyGlyLysGlySerLysGlySer		GUNGELEGAGGCCCAGGGGGCCCCAGGGGCTTCCAGGGCTTCCAGGGCCCAGGAGG GLYSerArgGLySerProGlyLysProGlyProGlnGlyProSerGlyAspProGlyPro 	ProGlyProProGlyLysGluGlyLeuProGlyProGluGlyProProGlyPheGluGly	LeugingiythrValgiyglu		GGCAGTCGAGGGAGGTGGGCCCCAAAGGCACCCAGGGTCCCAACGGCACCAGGGGTGTT	ProGlyValProGlyProArgGlyLeuProGlyLeuProGlyValProGly	Met	ATCACGGGGAAGCCGGGGAGTTCCGGGGAAGGAGGCCAGCGAGCAGCGCATCAGGGAGCTG	TGTGGGGGGATGATCAGGAACAAATTGCACAGTTAGCGGGGGCGCTTTG	ProGlyP	GCACCCGGGTCCATTGGTCGGCCCGGTCCAGGCTCCCTGGGCCCCCCAGGACCCCCA	GlyAlaVal-ValProLeuAlaLeuGlnAsnGluPro	פרו כרטו זמס זרשכיים מפכמים ייסטמ
STRANDEDN  TOPOLOGY:  MOLECULE TY FEATURE:  NAMEKEY:  LOCATION:	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity Query Match: DB:	US-09-763-7	Qy 142 V : Db 986 C	Qy 162 P Db 1031 G	Qy 182 G       Db 1091 G	Qy 202 I Db 1151 C	Oy 220 -	224	Qy 244 P	Oy 264 L       Db 1391 C	Oy 270 -	Db 1451 G	Qy 271 - Db 1511 C	288	1571		Oy 289 -	Db 1691 G	Oy 302 G	10/1

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1833 ------ GAAACCAGGGTGACAGGAGAAAG----- 1859
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314 -----ThrProAlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAs 331
                                                                                           331 pLysCysTyrTheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGl 351
                                                                                                                                                                                       351 uAspLysSerSerHisLeuValPheIleAsnThrArgGluGluGlnGlnTrpIleLysLy 371
                                                                                                                                                                                                                                                                                     371 sGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGl 391
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Patent No. 6127523

GENERAL INFORMATION:
APPLICANT: Brewton, Richard G.
APPLICANT: Brewton, Richard
TITLE OF INVENTION: TYPE IX COLLAGEN AND FRAGMENTS THEREOF
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: McGregor & Adler, LLP
STREET: 8011 Candle Lane
CITX: Houston
STATE: Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2032 CGACACCTCAGCCTGCCAGGAGCCGTGTTAGGAGGG 2068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 -----GluAspCysAlaGlyLeuIleTyrAlaGly 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5913D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEPHONE: (713) 777-6908
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 10.243 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 77071
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft WORD for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 47..2098
-073-663-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: unknown MOLECULE TYPE: CDNA
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-073-663-11
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1 1	391 1913	411 pAsnTrj 1972 GCCTCC	Oy 421GluAspOySAlaGLy Db 2032 CGACACCTCAGCTGCCAAGGA	KESULI 908-642-255-48 US-08-642-255-48 ; Sequence 48, Application US/08 ; Patent No. 577349	APPLICANT: CAPPELLO, JOSEE APPLICANT: FERRARI, France TITLE OF INVENTION: High M	⊶ 🖼 🧸	YE:	ZIP: 94111-4187 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compati		APPLICATION NUMBE FILING DATE:	CLASSLIATIONION 433  ATTORNEY/AGENT INFORMATION: NAME: NOWLAND, BETTFAM I	TELECOMMUNICATION INFORMATI TELECOMMUNICATION INFORMATI TELEPHONE: (415) 494-876	NI	SEQUENCE CHARACTERISTICS: ; SEGUENCE H 432 base pairs rvobe.	doub inear	; MOUECULE TIFE: OLDER HUCLE; DESCRIPTION: /desc = "sylus-08-642-255-48	Alignment Scores: 7.77e-16 Pred. No.: 412.50 Score: 412.50 Percent Similarity: 55.70%	Best Local Similarity: 53.69% Query Match: 16.37% DB:
Alignment Scores:	142 ValAspSer :::    986 CTCGATGGC	/ 162 ProArgGlyProArgGlyAspArgGlySerGlnGlyProProGlyProThrGlyAsnLys 181	/ 182 GlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGlyPro 201 	202 IleGlyProAladlyProProGlyGluArgGlyGlyLysGlySerLysGlySer 219 1111	/ 220GlnGlyProLys 223	/ 224 GlySerArgGlySerProGlyLysProGlyProGlnGlyProSerGlyAspProGlyPro 243 	/ 244 ProGlyProProGlyLysGluGlyLeuProGlyProGlnGlyProProGlyPheGlnGly 263	/ 264 LeuGlnGlyThrValGlyGlu	7 270 270	1451 GGCAGTCGAGGGGGCCCCAAAGGCACCCAGGGTCCCAACGGCACCAGCGGTGTT	1511 CAGGGTGTC	/ 288 Met 288 ::: > 1571 ATCACGGGGAAGCCGGGAGTTCCGGGGAAGGAGGCCAGCGAGCG	288	1631 TGTGGGGGGATGATCAGCGAACAAATTGCACAGTTAGCCGCGCACCTAAGGAAGCCTTTG 1690	1691 GCACCCGGGTCCATTGGTCGGCCCGGTCCAGCTGGCCCCCTGGGCCCCCAGGACCCCA	302 Glyalaval-ValProLeualaLeuGlnAsnGluPro	/ 314ThrProAlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAs 331 	331 pLysCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLysLeuPheCysGl     :::    :::     1833GAAACCAGGGTGACAGAGGAGAAGAAG
ининшон р	Oy Db	Oy Dp	QY	Oy Dp	Qy Dp	Oy Op	Qy Dp	Qy Dp	Qy	<b>a</b> a	3 B	QY Db	οy	qa ò	g d	QV Db	QQ	Qy Db

alPheileAsnThrargGluGluGlnGlnTrplleLysLy 371	432 80 ve: 3 : 57 . 3
rSerHisLeuv alGlyArgGluss alGlyArgGluss	Scores: 7.77e-16 Length: 412.50 Matches: 55.70% Conservativ Similarity: 53.69% Mismatches: 16.37% Indels: 16.37% Gaps:
351 UASPLY 1860 371 SGINME 1875 391 UTPLY 1913 CCCCAA 411 PASHTY 1972 GCCCCAA 421 42 -255-48 UERAL INFOR APPLICANT: 7171LE OF IN WHERE OF IN WHERE OF STATE APPLICANT: COMPUTER RE ADDRESSEE STATE COMPUTER RE MEDIUM TY COMPUTER TY NOTHER TY DESCUENT TY T	Sco: imil. imil. l Sil
Db 1860 Oy 371 sGlnmetVe Db 1875 Oy 371 sGlnmetVe Db 1875 Oy 391 uTrpLysT Db 1913 CCCCAGG Oy 411 pasnrrpG Oy 411 pasnrrpG Oy 421G Db 2032 CCACCCT CGC 840 App 1972 GCCTCCCG OY 421G Db 2032 CCACCCT CGC 840 App 1850 BB 1875G Db 2032 CCACCCT CGC 840 App 1850 BB 1870 BB 187	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari Query Match:
QY Q	Ali Pre Sco Per Bes Que DB:

STRANDEDNESS: single

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946 CCTCAGGGACCCCCCGGCATC---GCCTACGAGGGGGCGCCCAGGGCCCTCCCGGCCCCCA 1002
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Patent No. 5424408
GENERAL INFORMATION:
APPLICANT: Reeders, Stephen T., Morrison, Karen E., Hudson, Billy
APPLICANT: G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-763-712A-2_COPY_91_547 (1-457) x US-08-159-784-4 (1-3394)
                                                                                                                                                                                      156 LeuGlnGlyProProGlyProArgGlyProArgGlyAspArgGlySer----
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86
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42
58
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TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen
TITLE OF ENVENTION: Polynucleotides
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Connecticut
COUNTRY: U.S.A.
ZIP: 06510
COMPIER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800K storage
                                                                                    Conservative:
Mismatches:
Indels:
                                                         Length:
Matches:
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                                                        1.03e-14
409.00
48.98%
43.88%
16.23%
; TOPOLOGY: linear
US-08-159-784-4
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                                                                                                    Best Local Similarity:
Query Match:
                                                                                     Percent Similarity:
                                             Aliqnment Scores:
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350 CysGluAspLysSerSerHisLeuValPheIleAsnThrArgGluGluGlnGlnTrpIle 369
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    GlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyVal 273
                                                                                                                                                                                                                                                                                              652 GGACCA---CCTGGATCCGATGGCCTGCCAGGCTTGAAGGGGAAACC-TGGAGACACTGG 707
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                                           GGAAGCCCAGGCCCACCTGGTTCAGCTGGAGAACCAGGGATGCAAGGAGAACCCGGGCCC
                                                                                                              APPLICANT: Received Stephen T
APPLICANT: Morrison, Karen E
APPLICANT: Morrison, Karen E
APPLICANT: Morrison, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 951263A
CURRENT APPLICATION NUMBER: US/08/399,889B
CURRENT FILING DATE: 1995-03-07
EARLIER APPLICATION NUMBER: 07/621091
EARLIER FILING DATE: 1990-11-30
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Mismatches:
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402.50
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US-08-399-889-1
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Best Local Similarity:
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LOCATION: (1)
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LENGTH: 1416
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Mismatches:
Indels:
Gaps:
                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA: No. 5424408 applicable
ATTORNEY, AGENT INFORMATION:
NAME: Barth, Richard S.
REGISTRATION NUMBER: 28180
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Matches:
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                          SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/621,091G
FILLIG DATE: 11/30/90
                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 900983/RB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 972-1400
TELEFAX: (212) 370-1622
                 Macintosh OS7.0
                                                                                                                                                                                                                                                                                                           TELEX: 236268
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1416 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Double
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COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintos
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MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
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LIBRARY: BOVINE lens CDNA
CLONE: KMC15
POSITION IN GENOME: No. 5424
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Best Local Similarity:
Query Match:
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330 ThrAspLysCysTyrTyrPheSerValGluLysGluIlePheGluAspAlaLysLeuPhe 349
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CCAAAAGGACCACCTGGAGTACGTGGAGGAGCCTGGCACAGTGAAGATCATCTCCCTTCCA 471
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172 CCTCCAGGGAGTCCTGTAGAAGGCATAAAAGGAGACAAGGGGTTGATGGGAGAGCCTGGC 231
                                                                                                              ||||||| |||||| CAAAGAGGTCACCACGTATAGAGAGACATGGGGTCACCAGGTCATCGGGAGCACCA
                                                                                        GlyGlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLys
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Patent No. 6007980

GENERAL INFORMATION:
APPLICANT: Readers, Stephen T
APPLICANT: Morrison, Karen E
APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
TITLE OF INVENTION NUMBER: US/09/167,364
CURRENT FILING DATE: 1998-10-07
EARLIER RIPING DATE: 1998-10-07
EARLIER RIPING DATE: 1998-10-07
NUMBER OF SEQ ID NOS: 2.0
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NAME/KEY: CDS
LOCATION: (1)..(1416)
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LENGTH: 1416
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Alignment Scores:
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US-09-484-970B-4
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APPLICANT: Hudson, Billy G
TITLE OF INVENTION: Alpha-3 Chain Type IV Collagen Polypeptides
FILE REFERENCE: 95-1263-C
CURRENT APPLICATION NUMBER: US/09/439,897
CURRENT FILLNG DATE: 1999-11-12
NUMBER OF SEO ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                              US-09-763-712A-2_COPY_91_547 (1-457) x US-09-439-897-1 (1-1416)
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; LOCATION: (1)..(1416)
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                                    816 ITCICITICITIGIACAAGGAAAIGAACAAGCCCAIGGACAGGA----
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Mismatches:
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                                                                                                                                                                                                                                                                     APPLICANT: JONES, Karen A.
APPLICANT: Volkmuth, Wayne
APPLICANT: Walker, Michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 172
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Matches:
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; Patent No. 6426186
; GENERAL INFORMATION:
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OTHER INFORMATION: Incyte ID No.
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400.50
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320 AsnGlyCysPro 323 ||| || ||| 979 AGAGGGGACCCT 990

Oy Dp

Search completed: March 21, 2003, 12:34:17 Job time : 61.552 secs

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Sequence 762, App
Sequence 782, App
Sequence 3946, App
Sequence 2094, App
Sequence 2004, App
Sequence 206, App
Sequence 22, Appl
Sequence 27, App
Sequence 42, Appl
Sequence 42, Appl
Sequence 42, Appl
Sequence 388, App
Sequence 388, App
Sequence 1138, App
Sequence 255, Appl
Sequence 2118, Appl
Sequence 255, Appl
Sequence 2118, Appl
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Sequence 613, Appl
Sequence 613, Appl
Sequence 613, Appl
Sequence 613, Appl
Sequence 311, Appl
Sequence 331, Appl
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
US-09-919-497-6

US-09-954-456-762

US-09-954-456-782

US-09-980-107-3946

US-09-980-107-2094

US-09-80-107-2094

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US-09-925-299-206
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0S-09-919-947-7

0S-09-954-531-961

0S-09-964-8248-255

0 US-09-815-343-1517

0 US-09-925-302-64
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2 US-10-044-090-22
0 US-09-925-308-308
0 US-09-925-301-42
0 US-09-954-456-725
0 US-09-954-456-725
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US-09-978-697-613
US-09-998-697-613
US-09-998-189-613
US-10-174-590-331
US-10-174-590-331
US-10-175-78-331
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ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INVENTION: SECRETED PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 198, Application US/09745763
Patent No. US20020065394A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collins-Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McCoy, John M.
LaVallie, Edward R.
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Treacy, Maurice
Spaulding, Vikki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jacobs, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 219
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-MODEL-framet-pln.model -DEV=xlp
-MODEL-framet-pln.model -DEV=xlp
-G=CgnC_1/USPTO_Spool/US09763712/runat_14032003_100950_18119/app_query.fasta_1.1877
-DB=Published_Applications_NA -OFWT-fastap -SUFFIX=rnpb -MINNATCH=0.1
-LOOPCI_0 -LOOPDEXT=0 -UNITE=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFWT-pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLENEX=20000000000 -USR=-US09763712_EGCN_1 1_123 @runat 14032003_100950_18119
-NCPU=6 -LOPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-NCPU=6 -LOPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NGS_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THRRADS=1 -XGAPDP=10 -XGAPEXT=0.5 -FGAPDP=6
-FGAPEXT=7 -YGAPDP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 2274, Ap
Sequence 57, Appl
Sequence 57, Appl
                                                                                                                                                                             (without alignments)
1596.010 Million cell updates/sec
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                                                                                                                                                                                                                                                                                           ......EDVNNFICEKDRETVLSSAL 457
                                                                                                                                                        March 21, 2003, 08:23:12 ; Search time 222.049 Seconds
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/DESPUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/DESPUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
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Compugen Ltd.
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US-09-954-456-2274
US-09-924-340-57
US-09-992-600A-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of hits satisfying chosen parameters:
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                       version:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993
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Maximum DB seq length: 200000000
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Match Length DB
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Ygapop 10.0 ,
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Perfect score:
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                                                                                                                                                                                                                                                                                                  US-09-763-712A-2_COPY_91_547 (1-457) x US-09-745-763-198 (1-2930)
                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
           US/09/745,763
                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                    NO: 198
                                                                                                                                                                                                                                                                              Gaps:
                                                     NAME: Sprunger, Suzanne A. REGISTRATION NUMBER: 41,323 TELECOMMUNICATION INFORMATION:
          APPLICATION NUMBER: US/09,
FILING DATE: 18-Jun-2000
CLASSIFICATION: <Unknown>
                                                                                   TELEPHONE: (617) 498-8284
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 198:
                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID
                                                                                                                            LENGTH: 2930 base pairs
                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                          4.13e-130
2514.00
99.78%
99.78%
CURRENT APPLICATION DATA:
                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                           US-09-745-763-198
                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                   Query Match:
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Sequence 2274, Application US/09954456
; Sequence 2274, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Sets
TITLE OF INVENTION: Sets
FILE REFERENCE: 689209-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT APPLICATION NUMBER: US/60/233,617
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
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    GlyProLysGlySerArgGlySerProGlyLysProGlyProGlnGlyProSerGlyAsp
                                      1581 GGCCCCAAAGGCTCCCGTGGTTCCCCTGGGAAGCCCGGCCCTCAGGGCCCCAGTGGGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 rArgGluGluGlnGlnTrpIleLysLysGlnMetValGlyArg---GluSerHisTrpIl 381
                                                                                                                                                                                                                                                                                                                                                      460 GGACCAAAGGGAGACACTGGGCCAAGTGGACCTCCAGGACCTCCGGGTGTGCCTGGTCCA
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Mismatches:
Indels:
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Matches:
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2274
LENGTH: 1410
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474.50
49.678
36.278
18.838
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US-09-954-456-2274
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                    TYPE: DNA
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381 eGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGlyThrSerProAs 401
                                                                                    uAspCysAlaGlyLeuIleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspValAs 441
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                    1110 GAGCATGACTGATTCCAAGACAGAGGCAAGTTCACCTACCCCACAGGAGAGTCCCTGGT
                                       PTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGl
                                                                                                                                                                                       US-09-763-712A-2_COPY_91_547 (1-457) x US-09-924-340-57 (1-1133)
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Mismatches:
Indels:
Gaps:
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Matches:
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455.00
47.46%
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18.06%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: 5'UTR
LOCATION: 1..475
NAME/KEY: CDS
LOCATION: 476.964
NAME/KEY: 3'UTR
LOCATION: 965..1133
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LOCATION: 1118..1133
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Best Local Similarity:
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DB:
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                                           401
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LOCATION: 476..964

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; Sequence 6, Application US/09919497
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260 CCTGGATTCCCAGGCAAAGTTGGATCACCTGGCCCACCTGGCCCTCAAGCAGAAAGGGC 319
                                                                                  GlyPheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGlyLeu 279
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Publication No. US20030027161A1

GENERAL INFORMATION:
APPLICANT: Benjain, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: 31.US4 DLV
CURRENT FILING DATE: 2001-11-13
FRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR FILING DATE: 2001-08-06
PRIOR PLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-05-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 AlaValValProLeuAlaLeuGlnAsnGluPro---ThrProAlaPro 317
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                                                                                                                                           235 -----GlnGlyProSer-----
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ORGANISM: Homo sapiens
FEATURE:
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LOCATION: 1..475
FEATURE:
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US-09-992-600A-57
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Mismatches:
Indels:
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Matches:
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455.00
47.468
41.538
NAME/KEY: 3'UTR
LOCATION: 965..1133
FEATURE:
NAME/KEY: POLYA_Signal
LOCATION: 1101..1106
                                                                                                    NAME/KEY: polyA_site
LOCATION: 1118..1133
                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                   US-09-992-600A-57
                                                                                                                                                                      Alignment Scores:
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US-09-919-497-6
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GGTGACCGAGGCTCCCTGGAACTCAAGGATCTCCAGGAGCAAAAGGGGATGGGGGAATT 4631
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Patent No. US20020106662A1
GENERAL INFORMATION:
APPLICANT: Mutter, George L.
TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-763-712A-2_COPY_91_547 (1-457) x US-09-919-497-6 (1-6158)
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130
38
76
180
18
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Matches:
Conservative:
Mismatches:
                                                    FILE REFERENCE: 80801/7225
CURRENT APPLICATION NUMBER: US/09/919,497
CURRENT FILING DATE: 2001-07-31
PRIOR PPLICATION NUMBER: US 60/221,735
PRIOR FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.0
LENGTH: 6158
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LOCATION: (2434)...(2434)
OTHER INFORMATION: n = a, c, g or t/u
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30.81%
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ORGANISM: Homo sapiens
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Best Local Similarity:
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APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using C
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
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| TTGGATTGATCCTAACCAAGGTTGCTCAGGAGATTCCTTCAAAGTTTACTGTAATTTCAC 5086
                                                                                          692 CCAAAGGGTAACAAAGGCTCTACTGGACCCGCTGGCCAGAAAGGTGACAGTGGTCTTCCA 4751
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4632 CCTGGTCCTGCTGGTCCCTTAGGTCCACCTGGTCCTCCAGGCTTACCAGGTCCTCAAGGC 4691
                                                                                                                                       ---GlnTrpIleLysLysGlnMe 373
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1794 CCTTTACCAATCT------TGTCCTCCAAAAAAAGGA------
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CURRENT APPLICATION NUMBER: US/09/954.456
CURRENT FILING DATE: 2001-09-18
PRIOR FLING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
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PRIOR FILING DATE: 2000-09-27
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Mismatches:
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PRIOR APPLICATION NUMBER: US/60/235,840 PRIOR FILING DATE: 2000-09-27 PRIOR APPLICATION NUMBER: US/60/235,863 PRIOR FILING DATE: 2000-09-27 NUMBER OF SEQ ID NOS: 2276 SOFTWARE: Patentin version 3.0 SEQ ID NO 762
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                                                                                                                                                                                                 9.61e-17
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39.818
30.818
17.988
                                                                                                                                    NAME/KEY: misc_feature; OTHER INFORMATION: n=a,t,g
US-09-954-456-762
                                                                                                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                    Alignment Scores:
                                                                                      LENGTH: 6158
                                                                                                    TYPE: DNA
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GAPLICANT: Young, Paul
TITLE OF INVENTION:
TITLE OF INVENTION: Bets
FILE REFERENCE: 689290-76
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-20
PRIOR PILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-27
PRIOR PILING DATE: 2000-09-27
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SOFTWARE: PatentIn version 3.0
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US-09-954-456-782
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|GTGCCAAGGGTCTGACTGGAAGCCCTGGCAGCCCTGGTCCTGATGGCAAAACT----
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Matches:
Conservative:
Mismatches:
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Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: HORNE, Darci T.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TILLE OF INVENTION: Gene Expression Profiles in
FILE REPERENCE: 44921-508-W0
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
                                                                                                                    Indels:
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                                                                      1.11e-16
452.50
52.11%
46.48%
17.96%
                    TYPE: DNA
COCCANISM: Homo sapiens
US-09-954-456-782
                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-880-107-3946
SEQ ID NO 782
LENGTH: 6728
                                                               Alignment Scores:
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                                                                                                                                                                              ; OTHER INFORMATION: Genbank Accession No. US20020142981A1 274615
US-09-880-107-3946
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Mismatches:
Indels:
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Matches:
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR PILING DATE: 2000-16-137,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3946
LENGTH: 6728
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; Sequence 786, Application US/09954456
; Patent No. US20020115057A1
; GENERL INFORMATION:
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452.50
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Best Local Similarity:
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                                                                                                                                 TYPE: DNA
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3119 CTACCTGGTGTTGCTGTGTGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCT 3178
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                2699 AAAGGGCCTAAGGGTGAAAACGGTGTTGTTGGTCCCACAGGCCCCGTTGGAGCTGCTGGC
                                                                                            2759 CCAGCTGGTCCAAATGGTCCCCCGGTCCTGGAAGTCGTGGTGATGGAGGCCCCCT
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Fatent No. US20020142981A1

GENERAL INFORMATION:
APPLICANT: HORNE, Darci T.
APPLICANT: Gene Logic, Inc.
TILLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REPRENCE: 44921-5028-W0

CURRENT APPLICATION NUMBER: US/09/880,107

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14

PRIOR FILING DATE: 2000-06-14
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Conservative:
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2094
LENGTH: 5416
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Best Local Similarity:
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APPLICANT: YOUNG, Faul

TITLE OF INVENTION: Bets

FILE REBERBRUE: 689290-76

CURRENT APPLICATION NUMBER: US/09/954,456

CURRENT PELLOR DATE: 2001-09-18

PRIOR PELLORATION NUMBER: US/60/233,617

PRIOR PELLORATION NUMBER: US/60/234,052

PRIOR PELLORATION NUMBER: US/60/234,933

PRIOR PELLORATION NUMBER: US/60/234,933

PRIOR PELLORATION NUMBER: US/60/234,933

PRIOR PELLORATION NUMBER: US/60/235,134

PRIOR PELLORATION NUMBER: US/60/235,637

PRIOR PELLORATION NUMBER: US/60/235,637

PRIOR PELLORATION NUMBER: US/60/235,637

PRIOR PELLORATION NUMBER: US/60/235,637

PRIOR PELLORATION NUMBER: US/60/235,711

PRIOR PELLORATION NUMBER: US/60/235,711

PRIOR PELLORATION NUMBER: US/60/235,720

PRIOR PELLORATION NUMBER: US/60/235,730

PRIOR PELLORATION NUMBER: US/60/235,840

PRIOR APPLICATION NUMBER: US/60/235,840

PRIOR PELLORATION UNMBER: US/60/235,840
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110 AGAGGGTGCTGCTGGCATACCTGGAGGCAAGGGAGAAAAGGGTGAACCTGGTCTCAGAG
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SOFTWARE: PatentIn version 3.0
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Best Local Similarity:
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; Sequence 3947, Application US/09880107; Patent No. US20020142981A1; GENERAL INFORMATION:
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  NUMBER OF SEQ ID
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US-09-880-107-3947
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SEQ ID NO 104
LENGTH: 4149
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Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
CURRENT APPLICANTON US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.19
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Indels:
                                     NAME/KEY: unsure
LOCATION: 1492-1495, 1663, 1669, 4012, 4055
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                                                                        OTHER INFORMATION: a, t, c, g, or other
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257 ------GlyProProGlyPheGln 262
2609 GACCAAGGTCCAGTTGGCCGAACTGGAGAAGTAGGTGCAGTTGGTCCCCTGGCTTCGCT 2668
                                       2789 CTACCTGGTGTTGCTGGTGTGTGGTGAACCTGGTCTCTTGGCATTGCCGGCCCTCCT 2848
2489 GGTATGACTGGTTTCCCTGGTGCTGGTGGACGGACTGGTCCCCCCAGGACCCTCTGGTATT 2548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 206, Application US/09925299; Bublication No. US20030040617A9; Fublication No. US20030040617A9; GENERAL INFORMATION:
APPLICANT: ROSEON et al.; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies; FILE REFERENCE: PA102; CURRENT APPLICATION NUMBER: US/09/925,299; CURRENT FILING DATE: 2001-08-10; PRIOR APPLICATION NUMBER: PCT/US00/05883; PRIOR FILING DATE: 2000-03-08; PRIOR FILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 1556; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 206; LENGTH: 5145
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LOCATION: (5143)
OTHER INFORMATION: n equals a,t,g, or c
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ORGANISM: Homo sapiens
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LOCATION: (17)
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LOCATION: (5126)
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             APPLICANT: Scherf, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/231,379
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFFWARE: PATENTIN VET. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Genbank Accession No. US20020142981A1 Z74616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-763-712A-2_COPY_91_547 (1-457) x US-09-880-107-3947 (1-5086)
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Mismatches:
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Gaps:
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Matches:
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; LOCATION: (1).(5086)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-3947
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440.50
43.08%
35.85%
17.48%
  APPLICANT: Horne, Darci T.
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Query Match:
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LENGTH: 5086
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CURRENT APPLICATION NUMBER: US/09/925,299

CURRENT FILING DATE: 2001-08-10

PRIOR PLILING DATE: 2000-03-08

PRIOR FILING DATE: 1099-03-12
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Patent No. US20020055627A1
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OTHER INFORMATION: n equals a,t,g,
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LOCATION: (17)
OTHER INFORMATION: n equals
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 206
LENGTH: 5145
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LOCATION: (5126)
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GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL PROGram
SEQ ID NO 22
LENGTH: 5432
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43.388
17.488
; LOCATION: (5143)
; OTHER INFORMATION:
US-09-925-299-206
                                                                                                                                            Best Local Similarity:
Query Match:
                                                                                                                         Percent Similarity
                                                                        Alignment Scores:
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2283 GTCCTATTGGAAGCCGAGGTCCTTCTGGACCCCCAGGGCCTGATGGAAAGGGTGAAC 2342
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020137081A1 1383093.13
US-10-044-090-22
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Mismatches:
Indels:
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Matches:
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                                                                                         4.16e-16
440.50
43.08%
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ORGANISM: Homo sapiens
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Db 3122 CTACCAGGTGTTGGTGGTGAACCTGGTCTTTGGCGTCTCTTTGGCGTCTTTGGCGCCCTCT 3181

Qy 314 -------ThrProAlaProGluAspAsnG1yCysPro 323

Db 3182 GGGCCCGTGGTCTCCTGGTGGTAGTCTGGGTCAACGGTGCTCCT 3235

Search completed: March 21, 2003, 12:32:08

Job time: 248.049 secs
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Score
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516
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                            nucleic search, using frame_plus_p2n model
                                                                                                                                            16154066 segs, 8097743376 residues
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B248064 BB248064 BQ934501 AGENCOURT BQ71366 UI-M-FIO-BM713891 UI-E-EJO-BM713891 UI-E-EJO-BM9713891 UI-E-EJO-BM9713891 WI-E-EJO-BM9713891 WI-E-EJO-BM977436 CM4-HT024 AA012704 RPU1402CG AA304251 EST17006 AL543000 AL543000 BQ127513 if60106.y AA361740 EST14069 B1456015 603170460 BE929813 RC3-GN004 BQ955616 AGENCOURT BG681943 602629884 B1249235 602995511 BQ955927 AGENCOURT BQ713873 AGENCOURT B1456109 603172765 BQ891432 AGENCOURT BE910803 601661855 AL568743 AL568743 AW958053 EST370123 AW240221 up30b07.y BI697412 603348154 BC009162 Mus muscu BQ955927 AGENCOURT BQ674807 AGENCOURT BE290299 601089246 BQ887163 AGENCOURT W27610 35b6 Human Tetraodon BC013626 Mus muscu BQ921102 AGENCOURT pgf2c.pk0 AGENCOURT BB749743 BB749743 AV616076 AV616076 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description BQ921102 BM905999 BQ22234 BQ942234 BG171919 BM425818 BB613976 BG679800 BM809933 AL309697 SUMMARIES AW958053 BB248064 BQ934501 AA304251 AL543000 BQ127513 AA361740 B1697412 BQ887163 BQ955616 BG681943 BB749743 BC009162 AV616076 CNS04VYG BE929813 BG171919 BM425818 AW379436 AW240221 BQ222937 14 10 9 0110 4114 1144 010 010 14 Query Match Length DB 4444

ALIGNMENTS

3305 bp mRNA linear HTC 07-AUG-2002 Similar to scavenger receptor with C-type lectin, Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 3305) Strausberg, R.
Direct Submission clone IMAGE:2811487, mRNA. BC009162 BC009162.1 GI:14714370 Mus musculus, house mouse. Mus musculus BC009162 VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE REFERENCE

em\_gss\_mus:\* em\_gss\_other: em\_gss\_pro:\*

em\_gss\_rod:\*

ew\_gss\_pln:\* em\_gss\_vrt:\* em\_gss\_fun:\* em\_gss\_mam:\* e. .

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MetArgSerArgLeuAspThrGluValAlaAsnLeuSerValIleMetGluGluMetLys
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                                                                                                                                                                                                                    Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 5 Row: h Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis
This clone has the following problem: incomplete processing.
Submitted (05-JUN-2001) National Institutes of Health, Mammalian
                                                                                                                                                                        Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.
        Jene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
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417
24
16
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                                                                                                                       Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hqsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly'
Yoon, V.S., Kowis, C.R., Lawrence, S., Mart
Richards, S., Gibbs, R.A.
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                                             URL: http://mgc.nc1.nih.gov
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Matches:
Conservative:
Mismatches:
Indels:
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/clone="IMAGE:2811487"
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Eukaryota; Mactazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Muschabassa 1 to 957)

El (bases 1 to 957)

NIH-MGC http://mgc.nci.nih.gov/.

L Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.

CDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Llocation/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musinae; Musinae; Lo 861)
I (bases 1 to 861)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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CDNA Library Preparation: ResGen, Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://magge.llnl.gov

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/clone="IMAGE:6306240"
/clone_lib="NIH_MGC_129"
/lab_host="DH10B (phage-resistant)"
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Susan L. Sullivan, PhD.
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pCMV-SPORT6.1.ccdb; Site_1: EcoRV; Site_2: NotI; Cloned
unidirectionally. Primer: Oligo dT. Average insert size
2.2 kb. Constructed by ResGen, Invitrogen Corp. Note: this
is a NIH_MGC Library."
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Indels:
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Matches:
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91.01%
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                                         221
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
E. (Dases I to 906)
I. (Dipublished (1999)
I. Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDN Library Preparation: Life Technologies, Inc.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Preparation: Life Technologies, Inc.
CDN Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM11636 row: b column: 17
High quality sequence stop: 730.
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                                BI456109 906 bp. mRNA linear EST 21-AUG-2001 603172765F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:5251888 5',
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Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is an INH_MCC Library.
INIH_MCC Library.
250 c 244 g 163 t 6 others
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Mus musculus cDNA clone IMAGE:6332754
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                     195
                                                              362
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13790 row: n column: 19
High quality sequence start: 25
High quality sequence start: 25
High quality sequence stop: 632.
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                                                                                                                                     SerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLysProGln
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                                    GlyProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyPro
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy
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AGENCOURT_8754195 NIH_MGC_130
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234 ProGlnGlyProSerGlyAspProGlyProProGlyProProGlyLysGluGlyLeuPro 253
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/Clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
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AGENCOURT_8035172 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6212672
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 668)
NIH-MGC http://mgc.nci.nih.gov/.
NiH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can latter,//image.llnl.gov
Plate: LLCM377 row: c column: 09
High quality sequence stop: 656.
1. 668
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Tissue Procurement: ATCC
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BQ674807
BQ674807.1 GI:21785641
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
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                        1. .601
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/clone=lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
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Mus musculus cDNA clone IMAGE:3484163 5',
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys cDNA Library Preparation: Life Technologies, Inc.
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM8516 row: k column: 12
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552 bp mRNA linear EST 01-JUN-200
EST370123 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
AW958053
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Hegde, P., Oi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
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                  SerGluargGluasnGluTrpLysTrpLeuaspGlyThrSerProaspTyrLysAsnTrp
                                                 597 TCAGAGCGTGAAAATGAATGGAAGTGGCTGGATGGGACATCTCCAGACTACAAAATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assessment of gene expression patterns in a model of metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528
Fax: 301 838 0208
Email: john@etigr.org
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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, M
/note="Vector: pluescriptsKm"
112 c 143 g 121 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: placenta; Vector: pcwVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. Contact: Feng Liang Life Technologies. A maryland 20850, USA Fax: (1) 301 610 8371 Email: http://fulleqtech.com URL:

http://fulleqtch.invitrogen.com"

221 c 217 g 290 t 17 others
                              AL568743 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE005xH04 3 prime AL568743 LTI_FL002_PL1 Homo sapiens cDNA clone CS0DE005xH04 3 prime AL568743
                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 967)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization Unpublished (2001)
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BP 191 9106 EVRY cedex - France
Email: segreféquenoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xxef="Laxon:9606"
/clone="CSODE005xH04"
/clone_lib="LTL FL002_PL1"
/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases; 1 to 618)

2 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A.

3 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda

3 Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Rawai, J., Konno, H., Kouda

3 Hiramoto, K., Saito, R., Sakai, K., Sano, H., Sasaki

4 D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H.,

7 Takahi, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,

Muramatsu, M. and Hayashizaki, T., et al. 2001)

5 No Jul 6, 2000 this sequence version replaced gi:8940810.

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

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Tel: 81-45-503-9216

Fax: 81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y. and Hyashizaki,Y.
Computer-based methods for the mouse full-length cDNA
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Salto,T., Kiyosawa,B., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB248064 RIKEN full-length enriched, 7 days neonate cerebellum Mus musculus cDNA clone A730023E20 3', mRNA sequence.
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URL:http://genome.goc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
N., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
aggi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                AlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGluAspCysAlaGlyLeu 426
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                                                                                                  GluArgGluAsnGluTrpLysTrpLeuAspGlyThrSerProAspTyrLysAsnTrpLys
GlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAspSer
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AUTHORS
367
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BB248064
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SOURCE
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prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
                                                                         cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Labbratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], CDNA was
Computational Analysis of Full-Length Mouse cDNAs Compared with
                                                                                                                                                                                            1. .638
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="A730023E20"
/clone="A73002E20"
/clone="A73002E20"
                                Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                               /note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 ProAlaProGluAspAsnGlyCysProProHisTrpLysAsnPheThrAspLysCysTyr
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                    Genome. 12, 673-677
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Conservative:
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                                                                                                                                                                                                                                                                                                             /tissue_type="cerebellum"
/dev_stage="7 days neonate"
/lab_host="DH10B"
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AGENCOURT_8765685 NIH_MGC_130 Mus musculus cDNA clone IMAGE:6330794
5', mRNA sequence.
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Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                      L. Freeman
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/clone="IMAGE:6330794"
/clone=lib="NIH MGC_130"
/lab-host="DH10B (phage=resistant)"
/note="lorgon: otocysts; Vector: pCMV-SPORT6.1.ccdb;
Site_1: EcoRV; Site_2: Not1; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is in NIH MGC Library.

1 225 c 205 g 172 t
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Blossience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM13785 row: m column: 03
High quality sequence stop: 352.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 884)
NHH MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Matches:
Conservative:
Mismatches:
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie,
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798.50
90.24%
82.93%
31.69%
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                                                                                                                                                                                                                                                                            house mouse.
Mus musculus
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483 TCCATATTA 491
                                                                                                              SerAlaLeu 457
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AUTHORS
TITLE
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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. E. (bases 1 to 808)

NIH-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lonpublished (1999)

Lonpublished (1999)

Lonpublished (1999)

Tissue Procurement: Dr. Jim Lin, Gov Tissue Procurement: Dr. Jim Lin, Gov Tissue Procurement: Dr. Jim Lin, Dr. Mento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Libra at:

http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BQ771366 808 bp mRNA linear EST 26-JUL-2002 UI-M-FIO-byu-g-09-0-UI.rl NIH_BMAP_FIO Mus musculus cDNA clone IMAGE:5702432 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 GlyAsnLysGlyGlnLys-----GlyGluLysGlyGluPro---GlyProPro---Gly 194
120 uMetArgSerArgLeuAspThrGluValAlaAsnLeuSerVallleMetGluGluMetLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 nIleIleSerAsnIleSerTyrThrAlaHisHisLeuArgThrLeuThrSerAsnLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                        140 sLeuValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProPr
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/db_xref="taxon:10090"
/clone="INAGE:5702432"
/clone_lib="NIH_BMAP_FIO"
/tissue_type="whole brain"
/dev_stage="embryo 12.5dpc"
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BQ771366.1 GI:21979842
EST.
house mouse.
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(bases 1 to 500)

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Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                            Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                             Genome Res. 6 (9), 791-806 (1996)
                                               discovery
                                                                             97044477
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    /note="Organ: Brain: Vector: pXx-Asc; Site_1: ECOR I; Site_2: Not I; The library was constructed according Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel.First strand cDNA synthesis was primed with oligo-dr primer containing a Not I site. Double strand cDNA was size elected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pXx-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCACGAC. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator:"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 bp mRNA linear EST 27-FEB-2002 UI-E-EJO-ahq-c-05-0-UI.S2 UI-E-EJO HOMO Sapiens CDNA clone UI-E-EJO-ahq-c-05-0-UI.3', mRNA Sequence.
BM676508
BM676508.1 GI:18986404
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   368 TrplleLysLysGlnMetValGlyArgGluSerH1sTrplleGlyLeuThrAspSerGlu
/lab_host="DH10B (T1 phage resistant)"
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131
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Matches:
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93.33&
87.33&
30.44%
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Best Local Similarity:
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BM676508/c
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Chorozoe

Chartel and adult"

/ Jab_host="PubloB (Life Technologies) (TI phage resistant)"

/ Jab_host="DH10B (Life Technologies) (TI phage resistant)"

/ Anote="Organ: eye; Vector: pr713-pac (Pharmacla) with a
modified polylinker; Site_1: ECGR I; Site_2: Not I;

UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EGGR I adaptor, digested
with Not I, and cloned directionally into pT73-pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tags for this library are: fetal eyes, AGAATCAAGA
; lens, CGATTAAGTG; retina, CGGGG; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCFA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG_LIB=UT-E-EJO
TAG_LEB=UT-E-EJO
TAG_SEQ=AATGCGGATA
TAG_SEQ=AATGCCGGATA
TAG_SEQ=AATGCCGGATA
TAG_SEQ=AATGCCGGATA
TAG_SEQ=AATGCCGCATA
TAG_SEQ=AATGCCCGATA
TAG_TAGATA
TAG_SEQ=AATGCCCGATA
TAG_TAGATA
TAG_TA
                                                                                                                                                                                                                                      of Iowa
                                                                                                                                        Email: msoares@blue.weeg.ulowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iow
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seg primer: Mi3 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
        451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="UT-E-E-E-O-ahq-c-05-0-UI"
/clone_lib="UT-E-EJ0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
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Best Local Similarity:
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/dev.Stage="fetal and adult"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/lab_host="DH10B (Life Technologies) (TI phage resistant)"
/note="Organ: eye; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into PT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA
                                                                                                                                                                                                                                                                                                                                                                                                 DM/13891 ST 28-FEB-2002 UI-E-EJO-ahq-c-05-0-UI.rl UI-E-EJO Homo sapiens cDNA clone BM713891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 826
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="fetal eyes, lens, eye anterior segment, optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
                                                                                          380 TrplleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGlyThrSer 399
                       Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 443.498, >POLY_A#Simple_repeat
                                                                                                                                                                                                                                                                                                        440 ValAsnAsnPheIleCysGluLysAspArgGluThrValLeuSerSerAlaLeu 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .507
/organism="Homo sapiens"
/db_xref="taxon:966"
/clone="UJ-E-EJO'-ahq-c-05-0-UI"
/clone_lib="UJ-E-EJO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 6 (9), 791-806 (1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM713891.1 GI:19027149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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TITLE
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COMMENT
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KEYWORDS
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; lens, CGATTAGCGA; eye anterior segment, AATGCCGCAT; optic nerve, CCATTAAGTG; retina, CCGG; Retina Foveal an Macular, GTCC; RPE and Choroid, ACTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
                                                                                                                                                                                                                                                                               362 ThrargGluGluGlnGlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrpIle
                                                                                                                                                                                                                                                                                                                                                             402 TyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 TACAAAAATTGGAAAGCTGGACAGCGGGATAACTGGGGTCATGGCCCATGGGCCAGGAAA
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Matches:
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663.00
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                                                                              184
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                                                                                                                                                                                                        Query Match:
                                                                             BASE COUNT
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No
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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10 BC003705
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AB052103
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AC102618
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-MODEL=frame+_p2n.model -DEV=xlp
-MODEL=frame+_p2n.model -DEV=xlp
-Gegn2_1/USPTO_spool/US09763712/runat_14032003_100949_18101/app_query.fasta_1.1877
-DB=GenEmbl -OFWT=fastap -SUPFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=bicsum62 -TRANS=binman40 cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -MATRIX=DIO -THR_MIN-0 -ALIGEN=15 -MODE=LOCAL
-OUTRYT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09763712_@CGN_1_1_6828_@runat_14032003_100949_18101 -NCPU=6 -ICPU=3
-NO_XINLEXY -NO_MMAP -LARGEQUERS -NGS_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                             21, 2003, 06:54:47; Search time 3021.43 Seconds (without alignments) 4401.885 Million cell updates/sec
                                                                                                                                       2520
1 MNSQLNSFTGQMENITTISQ........EDVNNFICEKDRETVLSSAL 457
           GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
                                                                                                                            US-09-763-712A-2_COPY_91_547
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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9b_or:

9b_ph:

9b_ph:

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9b_pr:

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                                                                                                                                                                            BLOSUM62
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AC114677 Mus muscu AC107618 Mus muscu AC107618 Mus muscu AB007829 Homo sapi E32511 Scavenger r E32509 Scavenger r BC076446 Mus muscu AL845306 Danio rer AB1231 Rat pulmona AF053538 Alvinella

X490920 Sequence AB078434 Mus muscu AB038519 Mus muscu

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Description

AB038518 Homo sapi

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Homo sapi Rattus no

AL713657 Homo sapi

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AC112416 FAC112416 FAC102618 NAC102618 FAC016128 FAC016128

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AX334792 Sequence X65018 H.saplens m X75911 B.taurus mR AF509590 Bos tauru BC0022318 Homo sapi BC008760 Homo sapi E07265 CDNA encodi

BC003705 Mus muscu L40156 Mus musculu M76730 Chinese ham L06863 Cricetulus

U07973 Gallus gall

D90279 Human mRNA M76729 Human pro-a

AX146422 Sequence AX146424 Sequence AF137273 Gallus ga

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RLDSVSLRMQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGPFGPRGP
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Submitted (25-JUN-1997) Katsuki Ohtani, Asahikawa Medical College,
Department of Microbiology; 2-11-1 Midorigaoka-Higashi, Asahikawa,
Hokkaido 078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:+81-166-68-2393, Pax:+81-166-68-2399)
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KEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESHWIGLTDSERENEWKWLDG
TSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDFQCEDVNNFICEKDRETVLSS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The membrane-type collectin CL-Pl is a scavenger receptor of vascular endothelial cells
J. Biol. Chem. 276 (47), 44222-44228 (2001)
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Catarrhini; Hominidae; Homo.
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Bandman,O., Hillman,J.L., Tang,Y.T., Lal,P., Yue,H., E Lu,D.A. and Azimzai,Y.
Extracellular matrix and adhesion-associated proteins Patent: WO 0068880-A 39 16-NOV-2000;
Incyte Genomics, Inc. (US)
Location/Qualifiers
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Mammalia, Eutheria, Primates,
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3058 bp mRNA linear PRI 08-MAR-2001 for scavenger receptor with C-type lectin
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ATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATTATGGAAGAAATGAAG
                                                                                                                           LysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGly
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type I, complete cds.
AB038518
AB038518.1 GI:13365514
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/translation="MKDDFAEEEVQSFGYKRFGIQEGTQCTKCKNNWALKFSIILLY
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RANDTLEDMNSQLNSFTGQMENTTISGANEQNLKHDDLTSLNYLLANI
RADSVSLEMQQDLMRSRLDTEVANLSVTTGTDTLTKHTDDLTSLNYLLANI
RADSVSLEMQQDLMRSRLDTEVANLSVTTGTDTLTKHTDDLTSLNYLLANI
RGDRSQQPPROFTGROKGERGEPGPPGAERGFIGPROGFREG
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LFQVPGWPGPRGFPGPSGAVVPLALQMEPTPAPBDNSCYPCPHWKNTPSVPSVB
KEIFEDAKLFCEDKSSHLVPTNYFREDQWIKKQMVGRESHWTGLTDSRFRUNGKYFSVB
TSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQWNDFQCEDVNNFICEKDRETVLSS
                                                                                                1 (sites)
Makamura,K., Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura,T.
Molecular cloning and functional characterization of a human
scavenger receptor with C.type lectin (SRCL), a novel member of a
Scavenger receptor family
Biochem. Biophys. Res. Commun. 280 (4), 1028-1035 (2001)
                                                                                                                                                                                                                                                                         Direct Submission.

Direct Submission.

Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medical School, Division of Biochemistry, Biomedical Research Center; 2-2 yamadaoka, Suita, Osaka 565-0871, Japan

(E-mail:knakamurêonbich.med.osaka-u.ac.jp,

Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
                                   Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/gene="SRCL"
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/product="scavenger receptor with C-type lectin type
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/gene="SRCL"
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                              1424 ATGAGGTCGAGGTTAGACACTGAAGTAGCCAACTTATCAGTGATTATGGAAGAAATGAAG
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Db 433 AATAATACCCTGGCCAACATCCGTTTGGATTCTGTTTCTCTCAGGATGCAACAAGATTTG 492	MetargSerargLeuAspThrGluValAlaAsnLeuSerVallleMetGluGluMetLys 1	141		Qy 161 GlybroargGlyProArgGlyAspArgGlySerGlnGlyProProGlyProThrGlyAsn 180	Oy 181 LysGlyGlnLysGlyGluLysGlyGluProGlyProProGlyProAlaGlyGluArgGly 200	Qy         201 ProlleGlyProAlaGlyProProGlyGluArgGlyGlyLySGlySerGln         220           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 221 GlyProLysGlySerArgGlySerProGlyLysProGlyProGlnGlyProSerGlyAsp 240	241 ProGlyProProGlyProProGlyLySGluGlyLeuProGlyProGlnGlyProProGly	Oy 261 PheGlnGlyLeuGlnGlyThrValGlyGluProGlyValProGlyProArgGlyLeuPro 280	Qy 281 GlyLeuProGlyValProGlyMetProGlyProLysGlyProProGlyProProGlyPro 300	Qy 301 SerGlyAlaValValProLeuAlaLeuGlnAsnGluProThrProAlaProGluAspAsn 320	321 GlyCysProProHisTrpLysAsnPheThrAspLysCysTyrTyrPheSerValGluLys	Qy 341 GluIlePheGluAspAlaLysLeuPheCysGluAspLysSerSerHisLeuValPheIle 360	361 AShThrargGluGluGlnGlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrp	381 11eG1yLeuThrAspSerGluArgGluAsnGluTpLysTrpLeuAspG1yThrSerPro	Qy 401 AspTyrLysasnTrpLysalaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGly 420 	Qy 421 GludspCysAlaGlyLeulleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspVal 440	Qy 441 AsnAsnPhelleCysGluLysAspArgGluThrValLeuSerSerAlaLeu 457 	RESULT 5 AX490920 LOCUS AX490920 2005 bp DNA linear PAT 16-AUG-20
Oy 421 GluAspCysAlaGlyLeuIleTyrAlaGlyGlnTrpAsnAspPheGlnCysGluAspVal 440	2324	VY **1 ASIMASININETEC-YOLUMNYSASPARA GALUIIN VALDEUSELALDEU 45/ 	RESULT 4	AX454442 N Sequence 27 from Paten AX454442	AA454442.1 GI:Z1/13845 human. I Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,	Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J., Paoni,N.P., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I. and Ye,W. TITLE Compositions and methods for the diagnosis and treatment of	disorders involving angiogenesis JOURNAL Patent: WO 0208284-A 27 31-JNN-2002; Genentech, Inc. (US); Baker, Kevin P. (US); Ferrara, Napoleone (US); Gerber, Hanspeter (US); Gerittsen, Mary E. (US); Goddard,	ud il P at	FEATURES 1. (US) Location/Qualifiers source 12005 /organism="Homo sapiens"	/db_xref="taxon:9b06" BASE COUNT 606 a 493 c 491 g 415 t ORIGIN	Alignment Scores:  Pred. No.: 2.84e-81 Length: 2005 Score: 2487.00 Matches: 455 Percent Similarity: 99.56% Conservative: 0	 98.00.89 60.89 60.89	US-09-763-712A-2_COPY_91_547 (1-457) x AX45442 (1-2005) QY	134 ATGAACAGCCAGCTCATCATTCACAGGTCAGATGGAGAACATCACCACTATCTCTCAA 21 AlaAsnGluGlnAsnLeuLysAspLeuglnAspCeuHisLysAspAlaGluAsnArgThr	Db 194 GCCAACGAGCAGCAGCAGAACCTGCAGGACTTACACAAAGATGCAGAGAATAGAACA 253  Qy 41 AlaileLysPheAsnGlnLeuGluGluArgPheGlnLeuPheGluThrAspIleValasn 60  Dh 254 [	61 IleIleSerAsnIleSerTyrThrAlaHisHisLeuArgThrLeuThrSerAsnLeuAsn	81 GluValArgThrThrCysThrAspThrLeuThrLysHisThrAspAspLeuThrSerLeu 	3/4

PAT 16-AUG-2002

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Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
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                                                                                                                                                      Compositions and methods for the diagnosis and treatment of disorders involving angiogenesis
Patent: WO 0200690-A 27 03-JAN-2002;
Genentech, Inc. (US)
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                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GlyProLysGlySerArgGlySerProGlyLysProGlnGlyProSerGlyAsp
                                                                  CCAGGCCCCCCGGGGCCCACCAGCAAAGAGGACTCCCCGGCCCTCAGGGCCCTCCTGGC
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Ohtani,K., Suzuki,Y., Eda,S., Kawai,T., Kase,T.,
Sakai,Y., Fukuoh,A., Sakamoto,T. and Wakamiya,N.
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LEGVPGMPGPSFKGPPGPPGSGAMEPLALQNBPPTASSVNGCPPHWKNTDKCYYFSLE
KETFEDAKLPCEDKSSKLYFT NEEPLQANFPTASSSHWFGTDRGSPSEWKLDG
SPVDYKNWKAGQPDNWGSGHGPGEDCAGLIYAGQWNDPGCDFINNFICEKERENVPS
Direct Submission
Submitted (18-378-2002) Katsuki Ohtani, Asahikawa Medical College,
Wibinited (18-378-2002) Midorigaoka-Higashi, Asahikawa, Hokkaido
Microbiology; 2-1-1-1 Midorigaoka-Higashi, Asahikawa, Hokkaido
078-8510, Japan (E-mail:ohtani@asahikawa-med.ac.jp,
Tel:81-166-68-2393, Fax:81-166-68-2399)
Location/Qualifiers
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/protein_id="BAC05523.1"
/db_xref="G1:21901969"
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/tissue_lib="Liver"
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KEYWORDS
SOURCE
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musculus cDNA to mRNA

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/translation="MKDDFAEEEEVQSFGYKRFGIHEGTQCTKCINNWALKFSIVLLY
ILCALLTITVAILGYKVVEKMDNVSDGMETSHQTYDNKLTAVESDLKKLGDQAGKKAL
STNSELSTFRSDILDLEQQLQETTEKTSKNKDTLEKLQANGDSLVDROSGUKETLQNN
SFLITTOVNKTLQAY NGYVTHLQODTHVCGCHQSQSVTMNLINNLNLTQVQQRI
LISNLQOYDTSLATQRIKNDFQNLQQVFLQAKKDTPWLKEKVQSLQTLAANNSALA
KANNDTLEDMNSQLSSFTGQMNITTISQANEQSLKDLQDLHKDTENRTAVKFSQLEE
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RLDSISLRMQODMMRSKLDTEVANLSVVMEEMKLVDSKHGOLIKNFTILQGPPGPRGP
KGDRGSQGPPGPTGNKGQKGEKGEPGPPGPPGFRGTIGPVGPPGERGSKGSKGSQGPK
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LPGVPGMPGPKGPPGPPGPSGAMEPLALQNEPTPASEVNGCPPHWKNFTDKCYYFSLE
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SPVDYKNWKAGQPDNWGSGHGPGEDCAGLIYAGQWNDFQCDEINNFICEKEREAVPSS
                                                                 Nakamura,K., Funakoshi,H., Tokunaga,F. and Nakamura,T.
Molecular cloning of a mouse scavenger receptor with C-type lectin (SRCL)(1), a novel member of the scavenger receptor family Biochim. Biophys. Acta 1522 (1), 53-58 (2001)
21575692
2 (bases 1 to 3291)
                                                                                                                                                                                                                 Medical
nter; 2-2
                    Vertebrata; Euteleostomi;
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2 (bases I to 3291)

Nakamura,K. and Nakamura,T.

Direct Submission

Submitted (18-FEB-2000) Kenji Nakamura, Osaka University Medica School, Division of Biochemistry, Biomedical Research Center;; yamadaoka, Sulta, Osaka 565-0871, Japan (E-mail:Knakamur@obich.med.osaka-u.ac.jp,

Tel:81-6-6879-3783(ex.3783), Fax:81-6-6879-3789)
                                   Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product."scavenger receptor with C-type lectin."
/protein_id="BAB82497.1"
/db_xref="GI:18146952"
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/db_xref="taxon:10090"
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/gene="src1"
1 757 c
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77. .2305
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96.06%
90.81%
                Eukaryota; Metazoa;
                                     Mammalia; Eutheria;
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                                                                    AUTHORS
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         MetArgSerArgLeuAspThrGluValAlaAsnLeuSerValI1eMetGluGluMetLys
                                                                                                       LeuValAspSerLysHisGlyGlnLeuIleLysAsnPheThrIleLeuGlnGlyProPro
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                                                                 HSM802985 1886 bp mRNA linear PRI 20-MAR-2002
HOMO Sapiens mRNA; cDNA DKF2p547G1215 (from clone DKF2p547G1215).
AL713657
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
1. .1886
                                                                                                                                                                                                                                                                                      German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRESHWIGLIDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDCAGLIYAGQW
                                                                                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain"
/clone_lib="547 (synonym: hfbr1). Vector pSportl; host
DBH10B: sites NoII + SalI"
/dev_stage="fetal"
                                                                                                                                                                                                                                                  German Cancer
                                                                                                                                                                                                                                                                                               Genome Project.
This clone (DKFZp547G1215) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="DKFZp547G1215"
/note="similarity to asialoglycoprotein receptor (Mus
                                                                                                                                                                                (bases 1 to 1886)

Koehrer, K., Beyer, A., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submitssion

Submitted (12-MAR-2002) MIPS, Am Klopferspitz 18a, D-82152

Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cance Research Center (DKF2); Email s. Wiemann@&Kf2-heidelberg.de;
Berlin/Germany) within the cDNA sequencing consortium of the
1886
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Conservative:
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1838. .1843
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                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="18p11.3"
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1869
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/protein_id="Bab39148.1"
/db_xref="GI:13365553"
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Nakamura,K., Funakoshi,H., Miyamoto,K., Tokunaga,F. and Nakamura
Molecular cloning and functional characterization of a human
scavenger receptor with C-type lectin (SRCL), a novel member of
scavenger receptor family
                   1083 GACTACAAAAATTGGAAAGCTGGACAGCCGGATAACTGGGGTCATGGCCCATGGGCCAGGA 1142
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 AspTyrLysAsnTrpLysAlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGly
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Nakamura, K. and Nakamura, T.
Direct Submission
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                                   MetAsnSerGlnLeuAsnSerPheThrGlyGlnMetGluAsnIleThrThrIleSerGln
                                                                                                     21 AlaAsnGluGlnAsnLeuLysAspLeuGlnAspLeuHisLysAspAlaGluAsnArgThr
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qq	Db 1878 GCCAACCCCCAGTGTGGCCCCCACCCATGTTATTTTTTTT	
Qy	2y 320 320	Qy 320
qq	bb 1938 AGGGTCTCACTGTGCCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAACC 1997	m
Qy	Jy 320 320	320
qq	Db 1998 CCCACATCCCGGGTTCAAGTGATTCTCCTTGCCTTAGCCTCCCAGGTAGCTGGGAATACAA 2057	m
δy	λγ 320 320	320
qq	0b 2058 GCGTGTGCCCCCACAGCCAGGTAATTTTTGTATTTTTAGTAGAGGGGTTTCACAGTGT 2117	m
οy	yy 320 320	320
qq	30 2118 TGGGCAGGGTGGTTTCAAACTTCTGGCCTCAAGTGATCCACCTACCT	m
٥y	yy 320 320	320
QQ	Ob 2178 GCTGGGAATACAGGTGTGAACCACCACGTTTTGTCCCCCGGCTGCATATTAATTA	m
δλ	N 320 320	320
qq	Ob 2238 AAAGGCATCATAGGGGTTGGCACAGGAGCCCTGCTGCCAGAACAGGCCTCCATACCAGGC 2297	m
٥y	yy 320 320 320	321
qq	Db 2298 AIGTGTCTCTCTAAACGCCATTGGGTTTTTTAGTGCTCATTTGTTTTATGTATTATGT 2357	
ΟŊ	yy 320 320	329
q	0b 2358 GTGTATGTATGGGACAGGGTCTCACTCTGTCACCCAGGCTGGAATGACGAAGTGAAGTAG 2417	3438
ΟŊ	yy 320 320	349
qq	Ob 2418 IGCAAACATAGCICATIGCAGCITIGACCICCIGGGCITAGGIGAICTICCCACICAGAC 2477	3498
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Qy	уу 320 320 320	389
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Q	yy 320 320	409
QQ	b 2598 CAACCTCCTGCCTCAGTCTTGCAAAGTGCTGGGATTCCAGGTGGGAGCCACTGCACCTG 2657	3678
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qq	DD 2658 GCTCTTGCACTTGTTTATTAGGAGCCAGCCCTCAGAAGACAAACAA	3738
Qγ	yy 320 320	449
qa	b 2718 TITCCTTCAGGGAAGCCTGCTGGCCGCCCTGAGCGCTCTTCCCTCGTTTTACATCCTCAC 2777	DD 3798 AGG
οy	y 320 320	RESULT 10 AC112416
qq	0b 2778 TCTGGAGATAGATGGGCTCCCTCGGTTAGCTCCATCAACATGTGGAATGGAACCCTCTGCT 2837	LOCUS AC DEFINITION RE
Οy	yy 320 320	
QQ	D 2838 ATTGATGACTACATTTAATTTCTTTTTGAGAAAGGTGTTAGATGTTACGGTGCCTTCTAG 2897	KEYWORDS HT
Qy	jy 320 320	
qq	D 2898 TCTTTGATAATTAAACCTTTGGCAAAACTCGAATGTTTGGTTAGCAACCAAGCCTATTT 2957	13 X
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QQ	b 2958 FFCFCCCTTTGACCCAACCGCTATTCTACTTGATTTTGGTCGGTGAGGCCCGGGTTATT 3017	

QY         320           Db         3018           QY         320           Db         3078           QY         320           Db         3138           QY         320           Db         3198           QY         329           Db         3498           QY         349           QY         409           Db         3558           QY         409           Db         3558           QY         429           Db         3738           QY         429
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of 1103

unknown of 1587 unknown of 2191 unknown of 1505

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is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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contig of 12788 bp in length
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/db_xref="taxon:10116"
/clone="CH230-350K4"
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                                   Bouck, J., Bowle S., Burkell, R. Brown, B., Brown, B., Bryant, N. B., Bulbay, C., Burch, P., Burkell, C., Burch, D., Bathorne, S.R., David, R., Chen, G., Cov, C., Cov, H., D., Dathorne, S.R., David, R., David, C. D., Cox, C., Cov, H., D., Dathorne, S.R., David, R., David, R., David, C., Cox, C., Cov, H., D., Dathorne, S.R., David, R., David, R., David, R., David, R., David, R., David, R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H. H., Douthwaite, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Farntaguto, D., Flags, N., Fort, J., Escotto, M., Falls, T., Ferraguto, D., Flags, N., Fort, J., Escotto, M., Estils, T., Ferraguto, D., Flags, N., Holloway, C., Harlis, B., Harnindez, J., Garcia, A., Garrer, T., Garza, N., Gill, R., Harris, C., Harlis, K., Hart, Havid, M., Hale, S., Hamilton, K., Harris, C., Harris, K., Hart, Havid, R., Harris, C., Lichterge, C., Lieu, C., Liu, J., Liu, W., Louiseged, H., Liu, J., Li, Z., Lichterge, C., Lieu, C., Liu, J., Liu, W., Liu, M., Mai, J., Martinez, E., Massey, E., Mawhiney, E., Martin, R., Martin, R., Martinez, E., Massey, E., Mawhiney, E., Matchell, T., Mortson, N., Nuyeen, N., Nuyeen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwonu, G., Marten, E., Sonaike, T., Sparks, A., Stanley, H., Yange, S., Warten, R., Sadery, G., Taylor, C., Taylor, T., Taleris, R., Tameris, K., Taneris, K., Taneris, K., Taneris, K., Taneris, C., Wang, S., Warten, R., Warten, R., Warten, R., Warten, R., War
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NOTE: This is a 'working draft' sequence. It currently consists of 28 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jul 12, 2002 this sequence version replaced gi:20303233.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (21-FEB-2002) Human Genome Sequencing Center, Departmer of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 130763)
                    Bimage,K., Blankenburg,K., Bonnin,D.,
eva,M., Brown,E., Brown,M., Bryant,N.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
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Consensus quality: 113686 bases at least Q40
Consensus quality: 115729 bases at least Q30
Consensus quality: 117044 bases at least Q30
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Contact: hgsc-help@bcm.tmc.edu
------ Project Information
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Center: Baylor College of Medicine
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                          Benton, J.,
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qq	14207 GGACCACCTGGCCCCCCAG		qα	15287
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qq	14267 CCAACCCCAGCATCAGAGG	GGTAAGTCCAAATCATCCTTTTCAGCCAGAAATAAG	qa	15347
Qy	320	320	Qy	423
qq	14327 GCAGTGTGTAGGCTTGGCT	GCAGTGTGTGGCTTGGCTAAACCAGACCTCAGGAGTCCCCTAATTACACTTAATATCAG 14386	qq Q	15371
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qq	14507 CCAAGTACTTATTTCAAGC	CCAAGTACTTATTTCAAGCTATCCTGCACCGGCTGCTCCCTGACCATCCTTGTCTT 14566		
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QΩ	14567 TCTTCTTTCTCCTAGAAAC	TCTTCTTTCTCCTAGAAACAGACCATTCCATCAATTAACTCCATCAGTATGCAGATGGGG 14626	- C4 F3	JOURNAL
Qy	320	320	REF	REFERENCE AUTHORS
QΩ	14627 TTTCTGTGATAGACCACAC	TTTCTGTGATAGACCACACTCTGGTTTTGCTTAAGAAGCTGCTGTGGTGTCTGTC		
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qa	14687 GACCATTAAGTCTTCACAA	GACCATTAAGTCTTCACAAAACTCTGTTCTAGTTAGGAAACAAGCCATGTGGGTCACTCA 14746		
Qy	320	320		
qq	14747 IGCIGGICCAIGAACITIC	TGCTGGTCCATGAACTTTGGTTCTGAAGTACACTTGTTTACAAGCTCCAGCTGATCCAAG 14806		

Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarate, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Plerre, N., Hagos, B., Horton, L., Hulle, W., Illev, I., Johnson, R., Jones, C.,	JOURNAL Unpublished REFERENCE 2 (bases 1 to 182029) AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,	I Bir Mus	hou Mus Euk Mam	ION N DS	AC114677 182029 bp DNA linear HTG 10- NM Mus musculus clone RP24-213K19, WORKING DRAFT SEQUENCE, 10	RESULT. 11		423 CVSAlaGlVLA	15347	CC1	383 LeuThraspSerGluargGluasnGluTrpLysTrpLeuAspGlyThrSerProAspTyr 402   11   11   11   11   11   11   11	15227	Qy 367GlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrpIleGly 382	Db 15167 GAAGACAAATCTTCCCATCTCGTTTTCATAAACTCAAGAGGAACAGGTATGTCAGCTG 15226	Qy 351 GluAspLysSerSerHisLeuValPhelleAsnThrArgGluGluGln 366		331 AsplvsCvsTvrTvrPheSerValGluLvsGluIlePheGluAspAlaLvsLeuPheCvs 350		14987 TGAGGCTGTCACTTTGGTATCTTAAACATAGCTGAGGAAATGCAGAGTGCCTTTTTTT 1504	Оу 320 320	Db 14927 ACAACTGTGAACATCTGTCCATGTTCTGTACAGGGACACTCCATTGGCATGCAAGCAGTG 14986	Оу 320 320	Db 14807 ACTGACAATGAGTATCAGGGCCCACCCCACTTTCTTCTTCTGTCATTATAAAGCCTAAC 14866	Oy 320 320
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CCAACCCCAATCACAGCCTTTCCACACTGTGGTGTTCACTATTGTGTACTGTAAAATCC  ACAACTGTGAACATCTTCCAACATTGTTGTACAGGGACACTGCAAGTGCAACTGCAACTGCAACATTGTAAAAATTTTTTTT	CCAACCCCAATCACACCCTTCCACACTGTGTGTGTTCACTATTGTGTACTGTAAAATCC  ACAACTGTGAACATCTGTCATCTTCTTACAGGGACACTCATTGGCATGCAGGGGTG  TGAGGCTGTCACTTTGGTATCTTAAACATAGCTGGGAAATGCAGGGTGCATTTTTTT  TGAGGCTGTCACTTTGGTATCTTAAACATAGCTGGGAAATGCAGGGAACTCTTTTTTTT	CCAACCCCAATCACACCCTTCCACACTGTGTGTGTTCACTATTGTGTACTGTAAAATCC  ACAACTGTGAACATCTGTCATCTTACACAGGGACACTCCATTGCATGCA	CCAACCCAATCACAGCCTTTCCACACTGTGGTGTTCACTATTGTGTACTGTAAAATCC  ACAACTGTGAACATCTGTCATGTTCTTACAGGGACACTCCATTGGCATGCAAGCAGTG  TGAGGCTGTCACTTTGGTATCTTAAAACATAGCTGAGGAATGCCAGTTGGCATGCAAGCAGTG  TGAGGCTGTCACTTTGGTACTTTAAAACATAGCTGAGAAATGCCGCCTCACTGGAAGACTTCTTT  ASAATCTACACTTTAAAAACGTTACATTCCTAGGAATGCCGCCTCACTGGAAGAACTTCACA ASPLySCySTYTTYPPHSSerValGluLySGluIlePheGluAspAlaLySLeuPheCys [	CCAACCCAATCACAGCCTTTCCACACTGTGGTGTTCACTATTGTGTACTGTAAAATCC  ACAACTGTGAACATCTGTCCATGTTCTGTACAGGGACACTCCATTGGCATGCAAGCGTG  TGAGGCTGTCACTTTGTACATTCTTGTACAGGACACTCCATTGGCATGCAAGCGTGTTTTTTTT	CCAACCCCAATCACACCTTTCCACACTGTGGTGTTCACTATTGTGTACTGTAAATCC 1492	14867 CCAACCCAATCACGCCTTCCACACTGTGGTGTTCACTATTGTGTACTGTAAAATC 1492 320	14867 CCAACCCAATCACAGCCTTTCCACACTGTGTGTTACTATTGTGTACTGTAAAATCC 1492 320	14867 CCAACCCAATCACACCACTCCACACTGTGGTGTTCACTATTGTGTACTGTAAAATCC 1492 320	14867 CCAACCCAATCACACCACTCCACACTGTGGTGTTCACTATTGTGTACTGTAAATCC 1492 320	14867 CCAACCCAATCACACCACTGCTGTGGTGTTCACTATTGTGTACTGTAAAATCC 1492 320	14867 CCAACCCAATCACACCACTGCTGTGGTGTTCACTATTGTGTACTGTAAATCC 1492 320	14867 CCAACCCAATCACACCTTTCCACACTGTGGTGTTCATTGGTACTGTAAATCC 1492 320	14867 CCAACCCAATCACACCACTGCTGTGGTGTTCACTATTGTGTACTGTAAATCC 1492 320	14867 CCAACCCAATCACACCTGTCCACACTGTGGTGTTCATTGGTACTGTAAATCC 1492 320	14867   CCAACCCAATCACAGCCTTTCCACACTGTGTGTGTTTGTGTACTGTAAATCC   1492   320	14867 CCAACCCAATCACAGCCTTTCCACACTGTGTGTGTTTGTGTACTGTAAATCC 1492 320	14867 CCAACCCAATCACAGCCTTTCCACACTGTGTGGTGTTCACTATTGTGTACTGTAAAATCC 1492 320	14867 CCAACCCAATCACAGCCTTTCCACACTGTGTGGTGTTCACTATTGTGTACTGTAAATCC 1492 320	14867 CCAACCCAATCACAGCCTTTCCACACTGTGTGGTGTTCACTATTGTGTACTGTAAATCC 1492 320	14867 CCAACCCAATCACAGCCTTTCCACACTGTGTGTGTTCACTATTGTGTACTGTAAAATCC 1492 320	14867 CCAACCCAATCACAGCCTTTCCACACTGTGTGTGTTCACTATTGTGTACTGTAAAATCC 1492 320 320	14867 CCAACCCAATCACAGCCTTTCCACACTGTGTGTGTTCACTATTGTGTACTGTAAAATCC 1492		14807 ACTGACAATGAGTATCAGGGCCCACCCTTTCTTCTTCTTGTCATTATAAAGCCTAAC 1486
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100 bp f 2755 bp in length

contig of

contig of 951 bp in length

of 100 bp contig of 4803 bp in length

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173 GlyProProGlyProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyPro 192
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53237 69572: contig of 16246 bp in length
69573 69672: aga of 100 bp
69573 69121: contig of 19349 bp in length
89022 89121: gap of 100 bp
89122 128310: contig of 39189 bp in length
128411 128410: gap of 100 bp
                                                                                                                                                                                                       63: gap of 100 bp 36938: contig of 19575 bp in length
                                                                                                                                                                                                                                                               138: gap of 100 bp
53226: contig of 16188 bp in length
                                                                                                                                            9: gap of 100 bp
17263: contig of 8454 bp in length
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1052. .3806
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/note="assembly_fragment"
3907. .8709
/note="assembly_fragment"
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/note="assembly_fragment"
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53327. .69572
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/note="assembly_fragment"
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/note="assembly_fragment"
37484 c 36555 g 52844
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/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="RP24-213K19"
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8709: con
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                                                                                                                                                                                                                                                                                                                                                                                                               Signature, B., Linton, L., Nusbaum, C., Lander, E., Alli, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Brown, A., Camarata, J., Campopiano, A., Chang, J., Collins, S., Collymore, A., Cooke, P., DeArellan, K., Dear, K., Diaz, J.S., Dodge, S., Cooke, P., DeArellan, K., Dear, K., Diaz, J.S., Dodge, S., Gard, S., Gord, S., Goyette, M., Graham, L., Grand-Pherre, N., Hagos, B., Marchas, A., Kells, C., LaRocque, K., Lamazares, R., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Lavine, W., Illav, I., Macdonald, P., Macdonald, P., Marchan, S., Mathews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Mathews, C., McCatthy, M., McEwan, P., McKernan, K., Meldrim, J., Mathews, C., McCatthy, M., McEwan, P., McKernan, K., Meldrim, J., Mucol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollaray, V., Raymond, C. R., Reta, R., Rabeack, M., Riley, R., Rase, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Stolanovic, N., Strauss, N., Subramanian, A., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travis, M., Travis, N., Triglio, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Voung, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Submitted (10-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using Repeathmasker: html
Center: Whitehead Institute/ MIT Center for Genome Center Center Genome Center or Street, Cambridge, MI Center for Genome Center or Stree
McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D.,
Ollver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
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Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, Tarais, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                           Submitted (10-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 182029)
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This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
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Insert size: 181129; sum-of-contigs
Quality coverage: 8.0 in Q20 bases; agarose-fp
Quality coverage: 8.0 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
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901 others

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Conservative: Mismatches: Indels:

Gaps:

Length: Matches:

	17545	GTTCCTTCTGTGTTTTTTAAATCAACAGTTAAAACTTTACATTCCTA-GGATGTCCGCCT 47545	47487	qq
	324		319	٥y
REFERENCE AUTHORS	47486	GCATGCAAGTGGTACAAGGCTGTGACTTTGATATCTTAAACACAGCTGAGGAAATGCAGG	47427	qq
TONG GOOD TO THE PERSON OF THE	318		318	οy
TITLE	47426	TGTGCTGTACAGTCCACATCTGAGAACATCTGCCCGGGTTCTACACAGGGACACCCATTG	47367	Ω
	318		318	Οy
	47366	CGTCATAAAGCCTAGCCCAACCCAGTCCCACCTTTCTTCACTGTGTGTTTCACTGCTG	47307	QD
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	47306	AACCTCCAGCCGATCCAAGCCGACAGTGTATCAGAACCCACCC	47247	Op
	318		318	ολ
	47246	GTGTGGGTCCCTCATGCTGGTCCACAAGCCAGACTTTGGTTCTGAAGTGTGCTTATTTAC	47187	QQ
	318		318	٥y
	47186	TGCCTTTCTGTCTTTTGACAGAAGTCTTTTGCAAAACTATACTAGTTAGGAGCCAAGC	47127	Q
	318		318	ŏ
	47126	TGCAGATAGGGTTTCTGTGACAGAGTCCACATTCTGGTTTTGCTTAAGAAGCTGTTGTGG	47067	Q
AUTHORS	318		318	δy
JOURNAL	47066	CCTTCATCTTTCTTTCTTCCTTAGAAACAGACCATTTTATCAGTTAACTCCACCAGTA	47007	Q
AUTHORS	318		318	ΟŊ
acinadabad	47006	CCCCTGTACCCCAAATACTTCCTTCAAGATATTCTACACTGGCTGCTCCCTGACCATCCT	46947	Op
ORGANISI	318		318	οy
KEYWORDS COIDER	46946	TGTTCCTGCTTAGACATTATCAGGTCTCTACTCATTTAGATGAGCCAGGCCTTCAGAAGA	46887	a .
ACCESSION	318		318	δ
DEFINITION	46886	AAAACAGCAGGGACCCTGTGTATCCCTCTGGATGCTTCAGTGCTGTCACTCAGGACCCTG	46827	QQ
RESULT 12 AC102618	318		318	٥y
	46826	GAGGAATAAGGCAGTGTAGGCTTGGCTAAACCAACCCCCAGGAGTCCCCTAATTACAC	46767	qq
Qy 418	318		318	ò
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Qy 398	318	ProThrProAlaProGlu	313	ó
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Qy 378	40040	GIACCI GGACCI CGGGGGGI I GCCAGGGGI I GCCAGGGGI I GCCI GGGCCI AAG	0 0	3 (
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Qy 365	36586	CCIGGCCCICAGGGCCCICCIGGCIICCAGGGACIACAGGGCACIGIGGGCCIIGGA	7004	9
Db 47606	272	ProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGly	253	Š Š
Qy 345	46526	GGCCCTCAAGGACCTAGTGGGGACCCAGGACCACGGTCCACCAGGCAAGGATGGACTC	46467	Q
47	252	GlyProGlnGlyProSerGlyAspProGlyProProGlyProProGlyLysGluGlyLeu	233	δλ
0v 325				

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Direct, S. Severy, P. Sener, S. Tender, S. Ali, A., Allen, N., Bastien, V., Boguslavkiy, L., Boukhquiter, B. Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Bastien, V., Baguslavkiy, L., Boukhquiter, B. Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., DeWar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzlugh, W., Cade, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Jones, C., Kamat, A., Kartas, A., Kells, C., LaRocque, K., Liu, G., MacLen, C., Macchand, P., MacConald, P., Mador, J., Methews, C., McCarthy, M., McWan, P., McKernan, K., McPheeters, R., Meldrim, J., McCatthy, M., McWan, P., McKernan, K., McPheeters, R., Meldrim, J., Norman, C., Lander, C., Candride, M., X., Waman, D., Ye, W.J., Young, G., Sainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Allen, J., Zembek, L., Zimmer, A. and Zody, M.

Barrien, B., Nusbeum, C., Lander, E., Alli, A., Allen, N., Anderson, S., Rarreira, P., Fitzegerala, W., Cooke, P., Deare, C., Diaz, J., Chapan, J., Chapan, J., Chapan, J., Chapan, J., Chapan, J., Chapan, J., Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC102618 193208 bp DNA linear HTG 21-AUG-2002 Mus musculus clone RP23-426G16, WORKING DRAFT SEQUENCE, 11 unordered pieces.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
6 GAACAGGT-ATGATATGTCAGCTGCACACTTGGTTGGAGAAAACTATAATTTAGAGATA- 47723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 AGGAAGGCTGCAGTTTGCATGTTTTCCAGGTATATGAGATATATGAATTCAAA 47852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 AGTIATACTTGGAAATTGCATGCCTTTGAGAGAGTCAAAGAGATCAAA----- 47771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 ------AATTCATGGTCTCATAAACAA 47792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGly 397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 GlyProGlyGluAspCysAlaGlyLeuIleTyrAlaGlyGlnTrp---AsnAspPheGln 436
                                                                                                                                                                       5 AspAlaLysLeuPheCysGluAspLysSerSerHisLeuValPheIleAsnThrArgGlu 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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Birren, B., Nusbaum, C. and Lander, E.
Mus musculus, clone RP23-426G16
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COMMENT

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clone_lib="RPCI-23 Female Mouse BAC"
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/note="assembly_fragment"
                                                                                     1314. .3101
/note="assembly_fragment"
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                 Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Lindblad-Toh, K., Lindglad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., Macdonald, P., Major, J., Matthews, C., Marchy, M., Maylor, J., Maneus, L., Mihova, T., Maenga, Y., Murphy, T., Naylor, J., Murphy, T., Naylor, J., Maylor, J., Maylor, C., Nicol, R., Norbu, C., Norman, C. H., Phunkhang, P., Peterson, K., Phunkhang, P., Peterson, K., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Wol, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Lisepack, Submission

Lower Submission

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

Http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 198000; agarose-fp
Insert size: 192208; sum-of-contigs
Quality coverage: 8.8 in 020 bases; agarose-fp
Quality coverage: 9.1 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequencing vector: Plasmid; n/a; 100% of reads Sequencing vector: Plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 191397 bases at least Q30 Consensus quality: 191397 bases at least Q30 Consensus quality: 191862 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107451 107550: gap of 100 bp 107551 127842: contig of 20292 bp in length 127843 127942: gap of 100 bp 127943 150179: contig of 22237 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1214 1313; gap of 100 bp 100 bp 1312; gap of 100 bp 1314 1313; gap of 100 bp 1310; contig of 1788 bp in length 3202 6759; contig of 3558 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9035 9134: gap of 100 bp 9135 74024: contig of 64890 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24: gap of 100 bp 88784: contig of 14660 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88785 88884: gap of 100 bp 88885 107450: contig of 18566 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150180 150279; gap of 100 bp
150280 188446; coniig of 38167 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188447 188546; gap of 100 bp 188547 193208; contig of 4662 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: gap of 100 bp 9034: contig of 2175 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L19116
Center clone name: 426_G_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74025 74124:
74125 8878
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6860 90
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FEATURES

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97943 TITIALGITITA---GGTCCTCCTGGCCCCAGAGGTCCAAAAGGTGACAGAGGATCTCAG 97999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98420 CCAACCCCAGCATCAGAGGTCAACGGTAAGTCCAAATCGTCCTTCTCAGCTAGAATTGTG 98479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98120 AGCAAAGGATCCAAAGGCTCACAGGGTCCCAAAGGATCTCGTGGGTCCCCAGGGAAGCCT 98179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173 GlyProProGlyProThrGlyAsnLysGlyGlnLysGlyGluLysGlyGluProGlyPro 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 ProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrValGlyGluProGly 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GlyProProGlyProProGlyProSerGlyAlaValProLeuAlaLeuGlnAsnGlu 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 PheThrIleLeuGlnGlyProProGlyProArgGlyProArgGlyAspArgGlySerGln 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 ValProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMetProGlyProLys 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 GlyLysGlySerLysGlySerGlnGlyProLysGlySerArgGlySerProGlyLysPro
                                                                                                                                                                                                                                                                                                                                                                                           1000 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-763-712A-2_COPY_91_547 (1-457) x AC102618 (1-193208)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches:
                                                                                                                                                                                                                                                                                                                                                                         vector_side:right"
40174 c 40217 g 57157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
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                                                                           9135. .74024
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                                                                                                                      74125. .88784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProThrProAlaProGlu----
                                                                                                                                                                                                                                                                                                                                                        clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.23e-26
981.00
41.25%
38.21%
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	Οy	318 318	418	GlyProGlyGluAspCysAlaGlyLeuIleTyrAla
	Ор	98480 GAGGAATAAGGCAGTGTGAGGCTTGGCTAAACCAACCCCGAGGAGTCCCCTAATTACAC 98539	000	AGGAAGGCIGCAGITIGCATGGGCTITTICCAGGIA
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	qq	98540 AAAACAGGAGCCTGTGTATCCCTCTGGATGCTTCAGTGCTGTCACTCAGGACCCTG 98599	LOCUS	AC016128 169088 bp Homo sapiens chromosome 18 clone R
	δÿ	318 318	· ACCESSION	SEQUENCE, 8 unordered pieces. AC016128
	Dp	98600 TGTTCCTGCTTAGACATTATCAGGTCTCTACTCATTTAGATGAGCCAGGCCTTCAGAAGA 98659	VERSION KEYWORDS	
	δý	318	SOURCE	
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	δy	318 318	REFERENCE AUTHORS	<pre>1 (bases 1 to 169088) Birren, B., Linton, L., Nusbaum, C. an</pre>
	QQ	98720 CCTTCATCTTTCTTCTTCTCCTTAGAAACAGACCATTTATCAGTTAACTCCACCAGTA 98779	TITLE JOURNAL	Homo sapiens chromosome 18, clone Unpublished
	δλ	318 318	AUTHORS	Z (Dases 1 to 169088) Birren, B., Linton, L., Nusbaum, C.,
	ogo	98780 IGCAGATAGGGTTTCTGTGACAGAGTCCACATTCTGGTTTTGCTTAAGAAGCTGTTGTGG 98839		<pre>Baldwin,J., Barna,N., Beckerly,R., Brown,A., Castle,A., Colangelo,M.,</pre>
	δλ	318 318		COOKe, P., DeArellano, K., Dewar, K., Ferreira, P., FitzHugh, W., Forrest,
	qq	98840 TGCCTTTCTGTCTTTGACAGAAAGTCTTTTGCAAAACTATACTAGTTAGGAGCCAAGC 98899		Galagan, J., Gardyna, S., Grant, G., Howland, J.C., Johnson, R., Jones, C.
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	Óγ	318 318		Stojanovic, N.,
	qq	98960 AACCICCAGCCGAICCAAGCCGACAGIGIAICAGAACCCACCC	TITLE	Wyman, D., Ye, W.J., Zimmer, A. and Zo Direct Submission
	Qy	318 318	JOURNAL	Submitted (20-NOV-1999) Whitehead Research, 320 Charles Street, Camb
	QQ	99020 CGTCATAAAGCCTAGCCCAACCCAGTCCCTTTCTTCACTGTGTGTTTCACTGCTG 99079	COMMENT	On Sep 9, 2000 this sequence version All repeats were identified using
	Óγ	318 318		<pre>Smit, A.F.A. &amp; Green, P. (1996-199' http://ftp.genome.washington.edu/Rl</pre>
	pp	99080 TGTGCTGTACAGTCCACATCTGAGAACATCTGCCCGGGTTCTACAGAGGGACACCCATTG 99139		Center: Whitehead Institute/ M.
	δλ	318 318		Center code: WibR Web site: http://www-seg.wi.mii
	qq	99140 GCATGCAAGTGGTACAAGGCTGTGACTTTGATATCTTAAACACAGGTGAGGAAATGCAGG 99199		nce_sub ject Ir
	δy	31938pAsnGlyCysPropro 324		Center project name: L999 Center clone name: 324_G_2
	Q D	99200 GITCCTICTGTGTTTTTAAATCAACAGTTAAAACTTTACATTCCTA-GGATGTCCGCCT 99258		Sequencing vector: M13; M77815
	yo d	325 HistrDLysAsnPheThrAspLysCysTyrTyrPheSerValGluLysGlullePheGlu 344		Assembly program: Phrap; versi Consensus quality: 165522 bases
				Consensus quality: 10/246 base: Consensus quality: 16/1996 base: Incort size: 177000 agained
	qq			Insert size: 1/700, dayaros H Insert size: 168388; sum-of-col Quality coverage: 6.2 in Q20 b
		365 GluGlnGln		Quality coverage: 6.5 in Q20 b:
				* consists of 8 contigs. The true of is not known and their order in
2	Qy Dp	378 SerHisTrpIleGlyLeuThrAspSerGluArgGluAsnGluTrpLysTrpLeuAspGly 397 		* arbitrary. Gaps between the cont. * runs of N, but the exact sizes on * This record will be updated with
		ThrSerProAspTyrLysAsnTrpLysAlaGlyGlnPr		* as soon as it is available and tl * be preserved. * 17943: contig of 1794
	qq	99485		* 17944 18043: gap of 100 1 * 18044 22424: contig of 438

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C., Lander, E., Allen, N., Anderson, M., R., Boguslavkiy L., Boukhgalter, B., M., Collins, S., Collymore, A., K., Domino, M., Donelan, L., Doyle, M., Est, C., Funke, R., Gage, D., G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Macdonald, P., Marquis, N., Macdonald, P., Marquis, N., Connor, T., O'Connell, P., R., Roy, A., Santos, R., Severy, P., R., Subramanian, A., Talamas, J., iev, H., Vo, A., Wheeler, J., Wu, X., and Zody, M.
                                                                                                                            DNA linear HTG 09-SEP-2000
RP11-324G2 map 18, WORKING DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I Institute/MIT Center for Genome
bridge, MA 02141, USA
ion replaced gi:6649269.
RepeatMasker:
                                                                                                                                                                                                                                                                                                               iniata; Vertebrata; Euteleostomi;
arrhini; Hominidae; Homo.
                       ATGAGAGTATATGAATGAATTCAAA 99565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MIT Center for Genome Research
AlaGlyGlnTrp---AsnAspPheGln 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         t' sequence. It currently ue order of the pieces in this sequence record is outigs are represented as of the gaps are unknown. Ith the finished sequence d the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bases; agarose-fp
bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5; 100% of reads Dye; 100% of reads ion 0.960731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nit.edu
s@genome.wi.mit.edu
n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              uses at least 040
uses at least 030
uses at least 020
ifp
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                                                                                                                                                                                                                                                                                                                                                                               and Lander, E. PP11-324G2
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APUUU915 188439 bp DNA linear PRI 27-APR-2002
Homo sapiens genomic DNA, chromosome 18p clone:RPI1-720L2, complete
sequences.
                            153603 CCTGGGAAGCCCGGCCCTCAGGGCTCCAGTGGGGACCCAGGCCCCCGGGCCCACCAGGC 153544
                                                                           Db 153303 CCAGGGGACAGGGCAGTGCATGTGCTTGAGACTGAGCCCAACCCCCAGTGTGGCCCCA 153244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 153191 -GCCCAGGCTGGAGTGCAGTGGCGTGATCTCGGCTCACTGCAACCTCCACATCCCGGGTT 153133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Db 153012 TCAAACTCCTGGCCTCAAGTGATCCACCTACCTTAGTCTCCCAAAGTGCTGGGATTACAG 152953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 153132 CAAGTGATTCTCCTGCCTTAGCCTCCCAGGTAGCTGGGACTACAAGCGTGTGCCCCCACA 153073
                                                                                                                                                                                                                                                                                                                                 Db 153243 C----- 153231
       229 ProGlyLysProGlyProGlnGlyProSerGlyAspProGlyProProGlyProProGly 248
                                                                                                                                                                                                                                                                                                                                                                                                                                           325 sTrpLysAsnPheThrAspLysCysTyrTyrPheSerValGluLysGluIlePheGluAs 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345 pAlaLysLeuPheCysGluAspLysSerSerHisLeuValPheIleAsnThrArgGluGl 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        365 uGlnGlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAs 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385 pSerGluArgGluAsnGluTrpLysTrpLeuAspGlyThrSerProAspTyrLysAsnTr 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   405 pLys------AlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------AspPheGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Homo sapiens genomic DNA
Published Only in Database (1999)
                                                                                                                                                                                                                                                                                                uAspCysAlaGlyLeuIleTyrAlaGlyGln------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 153230 -TGTTTTTTTTTTTTTTTGAGACAGGGTCTCACTCTTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens DNA, clone: RP11-720L2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:20334314
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| 152952 GTGTGAG 152946
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|Db 153903 AATTIGGAGATTITATAAGAAAAATTATTCATAACTATCATTCACAGTGGATTICAT 153844
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22425 22524: gap of 100 bp 2252 38094: contig of 15570 bp in length 38095 38194: gap of 100 bp 38195 49220: contig of 11026 bp in length 49221 49320: gap of 100 bp 49321 66394: contig of 17074 bp in length 65395 66494: gap of 100 bp 66495 91692: contig of 25198 bp in length 9163 91792: gap of 100 bp 91793 120869: contig of 25198 bp in length 120870 120869: gap of 100 bp 120870 120869: contig of 48119 bp in length. Location/Qualifiers
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/clone_lib="RPCI-11 Human Male BAC"
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...tote="assembly_fragment
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/note="assembly_fragment"
38195. .49220
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49321. .66394
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/note="assembly_fragment"
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Matches:
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                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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E 2 (bases 1 to 188439)  S Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama.A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission  L Submitted (17-DEC-1999) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-2 Suchiro-Chou,Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:Battori@gsc.riken.go.jp, Vokohama, Kanagawa 230-0045, Japan (E-mail:Battori@gsc.riken.go.jp,) Tel:81-45-503-911, Fax:81-45-503-9170)  On Apr 26, 2002 this sequence version replaced gi:9188470. Location/Qualifiers  Corganism="Homo sapiens"  //chromosone="18" //map="18p" //map="18p" //map="18p" //map="18p" //map="18p"	4.52e-25 954.50 58.40% : 52.62% 37.88%	_91_547 (1-457) x AP000915 (1-188439)	ASDLeuServalIleMetGluGluMetLysLeuValAspSerLysHisGlyGln 148         ::::::        AATTIGGAGAITITAIAAGAAAAAATTAITCATAACTAICATICACAGIGGAITICAT 44965	LeulleLysasnPheThrIleLeuGlnGlyProProGlyProargGlyProargGlyAsp 168 ::: GTTGACACCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ArgGlySerGlnGlyProProGlyProThrGlyAsnLysGlyGlnLysGlyGluLysGly 188 	GlubroGlyproProGlyproAlaGlyGluArgGlyProIleGlyProAlaGlyPropro 208	GlygluargglyglyLysglySerLysGlySerGlnGlyProLysGlySerargGlySer 228 	ProGlyLysProGlyProGlnGlyProSerGlyAspProGlyProProGlyProProGly 248	LysGluGlyLeuProGlyProGlnGlyProProGlyPheGlnGlyLeuGlnGlyThrVal 268	GlyGluProGlyValProGlyProArgGlyLeuProGlyLeuProGlyValProGlyMet 288	ProGlyProLysGlyProProGlyProSerGlyAlaValValProLeuAla 308	LeuGinasnGluProThrProAlaProGluAspasnGly	CCAGGGGACAGGGCAGTGCATGAGCTGAGCCAACCCCCAGTGTGTGGCCCCA 44365
2 (bases 1 Hattori,M., Fujiyama,A., Direct Submi Submitted (1 and Chemical and Chemical (E-mail: hattr Tel:81-45-5C On Apr 26, 2 On Apr 26, 7 Or Apr 27 Or Apr	cores: .llarity: Similarity:	-712A-2_COPY_91	AsnLeuSerValll        :::: AATTTGGAGATTTT	LeuIleLysAsnPh ::: GTTGACACCTTTTT	ArgGlySerGlnGl 	GluProGlyProPr 	GlyGluArgGlyGl 	ProGlyLysProGl 	LysGluGlyLeuPr 	GlyGluProGlyVa 	ProGlyProLysGl 	LeuGlnAsnGluPr 	CCAGGGGGACAGG
THOR FLE JRNA SOUT SOUT	Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Query Match:	09-763	131	149	169	189	209	229	249	269	289	309	322
AUTH TITL JOUR COMMEN FEATUR S S BASE C ORIGIN	Alic Pre- Sco Per- Bes Que- DB:	-Sn	Qy Dp	Qy Db	çy da	දුරු ප්	S S	Qy	oy Op	Qy Db	Qy	Oy Dp	Oy Op

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Streen, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beda, F., Boquslavkiy, L., Bukhdralter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Follins, S., Collymore, A., Cooke, P., Ferreira, P., Fitzhudy, W., Forrest, C., Gage, D., Fenestor, J., Earreira, P., Fitzhudy, M., Graham, L., Karatas, A., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Klein, J., Landers, T., Langocque, K., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Liu, G., Looke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Mormon, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Ralwa, K., Regov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Taravers, M., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Myman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 11 clone RP11-179K3 map 11, LOW-PASS SEQUENCE SAMPLING.
ACO24368
ACO24368
HTG; HTGS PHRSFN
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1 (bases 1 to 71044)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 11, clone RP11-179K3
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Submitted (28-FEB-2000) Whitehead Institute/MIT Center for Genome
                                                                                                                                                  ---- 44313
                                                                                                                                                                                                                                                  44313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44312 -GCCCAGGCTGGAGTGCAGTGGCTCACTGCAACCTCCACTGCAACCTCCAGGGTT 44254
                                                                                                                                                                                                                                                                                                                                                                                                                                 : 1||::::: 44133 TCAAACTCCTGGCCTCAAGTGATCCACCTTAGTCTCCCAAAGTGCTGGGATTACAG 44074
                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                               345 pAlaLysLeuPheCysGluAspLysSerSerHisLeuValPheIleAsnThrArgGluGl 365
                                                                                                                                                                                                   365 uGlnGlnTrpIleLysLysGlnMetValGlyArgGluSerHisTrpIleGlyLeuThrAs 385
                                                                                                                                                                                                                                                                                           385 pSerGluArgGluAsnGluTrpLysTrpLeuAspGlyThrSerProAspTyrLysAsnTr 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 uAspCysAlaGlyLeuIleTyrAlaGlyGln------TrpAs 433
325 sTrpLysAsnPheThrAspLysCysTyrTyrPheSerValGluLysGluIlePheGluAs 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 n------AspPheGl 436
                                                                                                                                                                                                                                                                                                                                                                                                  pLys------AlaGlyGlnProAspAsnTrpGlyHisGlyHisGlyProGlyGl
                                                                                                                                44351 -TGTTTTGTTTTGAGACAGGGTCTCACTCTGTT-----
                                              HTG; HTGS_PHASEO.
Homo sapiens.
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Db 44073 GTGTGAG 44067
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AUTHORS
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COMMENT

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38663: contig of 691 bp in length
38763: gap of 100 bp
39449: contig of 686 bp in length
39449: contig of 686 bp in length
                                                                                                                                                                                                                                                                              91: gap of 100 bp
25881: contig of 690 bp in length
81: gap of 100 bp
26774: contig of 693 bp in length
74: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                             27563: contig of 689 bp in length
27653: gap of 100 bp
28355: contig of 692 bp in length
28455: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                  28455: gap of 100 wp
29145: contig of 690 bp in length
29245: gap of 100 bp
29943: contig of 698 bp in length
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692 bp in length
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670 bp in length
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685 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440:36 contig of 687 bp in length 440236; contig of 689 bp in length 41025; contig of 689 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18: gap of 100 bp
42608: contig of 690 bp in length
08: gap of 100 bp
43399: contig of 691 bp in length
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9 33998: contig of 684 bp ir

9 33998: gap of 100 bp

3 4594: contig of 696 bp ir

5 34794: gap of 100 bp

5 35486: contig of 692 bp ir
                                                                                                                                                            100 bp
694 bp
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f 706 bp
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697 bp
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f 691 bp
                                                                                 ap of 100 bp contig of 693 bp
                                                                                                                   17: gap of 100 bp 22815: contig of 698 bp
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30745: contig of 702 bp
30845: gap of 100 bp
31535: contig of 690 bp
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48123: contig of 687 bp
23: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41125: gap of 100 bp 41818: contig of 693 bp
    2 19721: gap of 10
2 20425: contig of 7
6 20525: gap of 10
6 21224: contig of 6
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19450 39549: gap o.
19650 40236: cont.19 of
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44169: contig of
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* sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                        10 11809; gap of 100 bp 12 1211; contig of 702 bp in length 12 12611; gap of 100 bp 10 13304; contig of 693 bp in length 15 13404; gap of 100 bp 100 
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16460: contig of 686 bp in length
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Search completed: March 21, 2003, 11:17:28 Job time: 3321.43 secs

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